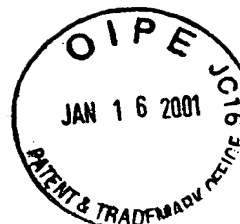


SEQUENCE LISTING



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<110> Zuker, Charles S.  
Adler, Jon Elliot  
Ryba, Nick  
Mueller, Ken  
Hoon, Mark  
The Regents of the University of California  
The Government of the United States of America  
as represented by the Secretary of the  
Department of Health and Human Services

<120> T2R, a Novel Family of Taste Receptors

<130> 02307E-098010US

<140> US 09/510,332

<141> 2000-02-22

<150> US 09/393,634

<151> 1999-09-10

<160> 172

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20 25 30

Ile Asp Leu Ile Lys His Arg Lys Met Ala Pro Leu Asp Leu Leu Leu  
35 40 45

Ser Cys Leu Ala Val Ser Arg Ile Phe Leu Gln Leu Phe Ile Phe Tyr  
50 55 60

Val Asn Val Ile Val Ile Phe Phe Ile Glu Phe Ile Met Cys Ser Ala  
65 70 75 80

Asn Cys Ala Ile Leu Leu Phe Ile Asn Glu Leu Glu Leu Trp Leu Ala  
85 90 95

Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Val Ala Ser Val Arg His  
100 105 110

Pro Leu Phe Ile Trp Leu Lys Met Arg Ile Ser Lys Leu Val Pro Trp  
115 120 125

Met Ile Leu Gly Ser Leu Leu Tyr Val Ser Met Ile Cys Val Phe His  
130 135 140

Ser Lys Tyr Ala Gly Phe Met Val Pro Tyr Phe Leu Arg Lys Phe Phe  
 145 150 155 160

Ser Gln Asn Ala Thr Ile Gln Lys Glu Asp Thr Leu Ala Ile Gln Ile  
 165 170 175

Phe Ser Phe Val Ala Glu Phe Ser Val Pro Leu Leu Ile Phe Leu Phe  
 180 185 190

Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met  
 195 200 205

Arg Asn Thr Val Ala Gly Ser Arg Val Pro Gly Arg Gly Ala Pro Ile  
 210 215 220

Ser Ala Leu Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Phe Ser His  
 225 230 235 240

Cys Met Ile Lys Val Phe Leu Ser Ser Leu Lys Phe His Ile Arg Arg  
 245 250 255

Phe Ile Phe Leu Phe Phe Ile Leu Val Ile Gly Ile Tyr Pro Ser Gly  
 260 265 270

His Ser Leu Ile Leu Ile Leu Gly Asn Pro Lys Leu Lys Gln Asn Ala  
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 290 295

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 tgtgttttcc atagcaaata tgcagggttt atggtcccat acttccctaag gaaatttttc 480  
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 ggtgcaccca tcagcgcgtt gctgtctatc ctgtccttcc tgatcctcta cttctccac 720  
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 Cys Asn Glu Leu Ile Lys His Arg Lys Leu Met Pro Ile Gln Ile Leu  
 35 40 45  
 Leu Met Cys Ile Gly Met Ser Arg Phe Gly Leu Gln Met Val Leu Met  
 50 55 60  
 Val Gln Ser Phe Phe Ser Val Phe Phe Pro Leu Leu Tyr Val Lys Ile  
 65 70 75 80  
 Ile Tyr Gly Ala Ala Met Met Phe Leu Trp Met Phe Phe Ser Ser Ile  
 85 90 95  
 Ser Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile  
 100 105 110  
 Ser Gly Phe Thr Gln Ser Cys Phe Leu Trp Leu Lys Phe Arg Ile Pro  
 115 120 125  
 Lys Leu Ile Pro Trp Leu Phe Trp Glu Ala Phe Trp Pro Leu Xaa Ala  
 130 135 140  
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 145 150 155 160  
 Ala Leu Arg Asn Thr Thr Leu Lys Lys Ser Lys Thr Lys Ile Lys Lys  
 165 170 175  
 Ile Ser Glu Val Leu Leu Val Asn Leu Ala Leu Ile Phe Pro Leu Ala  
 180 185 190  
 Ile Phe Val Met Cys Thr Ser Met Leu Leu Ile Ser Leu Tyr Lys His  
 195 200 205  
 Thr His Arg Met Gln His Gly Ser His Gly Phe Arg Asn Ala Asn Thr  
 210 215 220  
 Glu Ala His Ile Asn Ala Leu Lys Thr Val Ile Thr Phe Phe Cys Phe  
 225 230 235 240  
 Phe Ile Ser Tyr Phe Ala Ala Phe Met Thr Asn Met Thr Phe Ser Leu  
 245 250 255  
 Pro Tyr Arg Ser His Gln Phe Phe Met Leu Lys Asp Ile Met Ala Ala  
 260 265 270  
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 aagctaattgc caattcaaatt cctcttaattg tgcataaggga tgtctagatt tgggtctgcag 180  
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 atttatgggtg cagcaatgat gttcctttgg atgtttttta gctctatcag cctatgggttt 300  
 gccacttgcc tttctgtatt ttactgcctc aagatttcag gcttcaactca gtcctgtttt 360  
 ctttggttga aattcaggat cccaaagtta ataccttggc tgcttctggg aagcgttctg 420  
 gcctctgtga gcattgcac tgtgtgtcga ggtagattac gctaaaaatg tggaagagga 480  
 tgccctcaga aacaccacac taaaaaagag taaaacaaag ataaagaaaa ttagtgaagt 540  
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 ctttatttct tattttgctg ctttcatgac aaatatgaca tttagtttac cttacagaag 780  
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 Ser Ser Trp Phe Lys Thr Lys Arg Met Ser Leu Ser Asp Phe Ile Ile  
 35 40 45  
 Thr Thr Leu Ala Leu Leu Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr  
 50 55 60  
 Asp Ser Phe Leu Ile Glu Phe Ser Pro Asn Thr His Asp Ser Gly Ile  
 65 70 75 80  
 Ile Met Gln Ile Ile Asp Val Ser Trp Thr Phe Thr Asn His Leu Ser  
 85 90 95



Ile Trp Leu Ala Thr Cys Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala  
 100 105 110  
 Ser Phe Ser His Pro Thr Phe Leu Trp Leu Lys Trp Arg Val Ser Arg  
 115 120 125  
 Val Met Val Trp Met Leu Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser  
 130 135 140  
 Thr Ala Ser Leu Ile Asn Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly  
 145 150 155 160  
 Ile Glu Ala Thr Arg Asn Val Thr Glu His Phe Arg Lys Lys Arg Ser  
 165 170 175  
 Glu Tyr Tyr Leu Ile His Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro  
 180 185 190  
 Leu Ile Val Ser Leu Ala Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly  
 195 200 205  
 Arg His Thr Arg Gln Met Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro  
 210 215 220  
 Thr Thr Glu Ala His Lys Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe  
 225 230 235 240  
 Phe Leu Phe Leu Leu Tyr Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly  
 245 250 255  
 Asn Phe Leu Pro Lys Thr Lys Met Ala Lys Met Ile Gly Glu Val Met  
 260 265 270  
 Thr Met Phe Tyr Pro Ala Gly His Ser Phe Ile Leu Ile Leu Gly Asn  
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<212> DNA

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 attatcttga ctgatagttt tttaatagaa ttctctccca acacacatga ttcagggata 240  
 ataattgcaa ttattgatgt ttctggaca ttacaaacc atctgagcat ttggcttgcc 300  
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 tctgtggta gtaccgcac tctgatcaat gagtttaagc tctattctgt ctttagggga 480  
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tccagagatc caaccactga ggcccacaag agggccatca gaatcatcct ttccttcttc 720
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aaaaccaaga tggctaagat gattggcgaa gtaatgacaa tgttttatcc tgctggccac 840
tcattttattc tcattctggg gaacagtaag ctgaagcaga catttgtagt gatgctccgg 900
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<213> Homo sapiens

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<223> human T2R04 (hGR04)

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Lys Thr Trp Val Lys Ser His Arg Ile Ser Ser Ser Asp Arg Ile Leu
      35             40             45

Phe Ser Leu Gly Ile Thr Arg Phe Leu Met Leu Gly Leu Phe Leu Val
      50             55             60

Asn Thr Ile Tyr Phe Val Ser Ser Asn Thr Glu Arg Ser Val Tyr Leu
      65             70             75             80

Ser Ala Phe Phe Val Leu Cys Phe Met Phe Leu Asp Ser Ser Ser Val
      85             90             95

Trp Phe Val Thr Leu Leu Asn Ile Leu Tyr Cys Val Lys Ile Thr Asn
      100            105            110

Phe Gln His Ser Val Phe Leu Leu Leu Lys Arg Asn Ile Ser Pro Lys
      115            120            125

Ile Pro Arg Leu Leu Leu Ala Cys Val Leu Ile Ser Ala Phe Thr Thr
      130            135            140

Cys Leu Tyr Ile Thr Leu Ser Gln Ala Ser Pro Phe Pro Glu Leu Val
      145            150            155            160

Thr Thr Arg Asn Asn Thr Ser Phe Asn Ile Ser Glu Gly Ile Leu Ser
      165            170            175

Leu Val Val Ser Leu Val Leu Ser Ser Ser Leu Gln Phe Ile Ile Asn
      180            185            190

Val Thr Ser Ala Ser Leu Leu Ile His Ser Leu Arg Arg His Ile Gln
      195            200            205

Lys Met Gln Lys Asn Ala Thr Gly Phe Trp Asn Pro Gln Thr Glu Ala
      210            215            220

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His Val Gly Ala Met Lys Leu Met Val Tyr Phe Leu Ile Leu Tyr Ile  
 225 230 235 240  
 Pro Tyr Ser Val Ala Thr Leu Val Gln Tyr Leu Pro Phe Tyr Ala Gly  
 245 250 255  
 Met Asp Met Gly Thr Lys Ser Ile Cys Leu Ile Phe Ala Thr Leu Tyr  
 260 265 270  
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 Thr Thr Ala Lys Lys Ile Leu Cys Phe Lys Lys  
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 atctcctctt ctgataggat tctgttcagc ctgggcatca ccaggtttct tatgctggga 180  
 ctatttctgg tgaacacccat ctacttcgtc tcttcaaata cggaaagggtc agtctacctg 240  
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 actacgagaa ataacacatc atttaatatc agtgagggca tcttgctttt agtggtttct 540  
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 Arg Glu Trp Ile Arg Lys Phe Asn Trp Ser Ser Tyr Asn Leu Ile Ile  
 35 40 45

Leu Gly Leu Ala Gly Cys Arg Phe Leu Leu Gln Trp Leu Ile Ile Leu  
 50 55 60  
 Asp Leu Ser Leu Phe Pro Leu Phe Gln Ser Ser Arg Trp Leu Arg Tyr  
 65 70 75 80  
 Leu Ser Ile Phe Trp Val Leu Val Ser Gln Ala Ser Leu Trp Phe Ala  
 85 90 95  
 Thr Phe Leu Ser Val Phe Tyr Cys Lys Lys Ile Thr Thr Phe Asp Arg  
 100 105 110  
 Pro Ala Tyr Leu Trp Leu Lys Gln Arg Ala Tyr Asn Leu Ser Leu Trp  
 115 120 125  
 Cys Leu Leu Gly Tyr Phe Ile Ile Asn Leu Leu Leu Thr Val Gln Ile  
 130 135 140  
 Gly Leu Thr Phe Tyr His Pro Pro Gln Gly Asn Ser Ser Ile Arg Tyr  
 145 150 155 160  
 Pro Phe Glu Ser Trp Gln Tyr Leu Tyr Ala Phe Gln Leu Asn Ser Gly  
 165 170 175  
 Ser Tyr Leu Pro Leu Val Val Phe Leu Val Ser Ser Gly Met Leu Ile  
 180 185 190  
 Val Ser Leu Tyr Thr His His Lys Lys Met Lys Val His Ser Ala Gly  
 195 200 205  
 Arg Arg Asp Val Arg Ala Lys Ala His Ile Thr Ala Leu Lys Ser Leu  
 210 215 220  
 Gly Cys Phe Leu Leu Leu His Leu Val Tyr Ile Met Ala Ser Pro Phe  
 225 230 235 240  
 Ser Ile Thr Ser Lys Thr Tyr Pro Pro Asp Leu Thr Ser Val Phe Ile  
 245 250 255  
 Trp Glu Thr Leu Met Ala Ala Tyr Pro Ser Leu His Ser Leu Ile Leu  
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 tggtcctcat ataacctcat tatcctgggc ctggctggct gccgatttct cctgcagtgg 180

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Arg Gly Trp Val Lys Lys Met Xaa Gly Val Pro Ile Asn Ser His Asp
      35           40           45
Ser Gly Lys Xaa Pro Leu Ser Pro Thr Gln Ala Asp His Val Gly His
      50           55           60
Lys Ser Val Ser Thr Phe Pro Glu Gln Trp Leu Ala Leu Leu Ser Xaa
      65           70           75           80
Cys Leu Arg Val Leu Val Ser Gln Ala Asn Met Xaa Phe Ala Thr Phe
      85           90           95
Phe Ser Gly Phe Cys Cys Met Glu Ile Met Thr Phe Val Xaa Xaa Xaa
      100          105          110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      115          120          125
Xaa Leu Leu Val Ser Phe Lys Ile Thr Phe Tyr Phe Ser Ala Leu Val
      130          135          140
Gly Trp Thr Leu Xaa Lys Pro Leu Thr Gly Asn Ser Asn Ile Leu His
      145          150          155          160
Pro Ile Leu Asn Leu Leu Phe Leu Xaa Ile Ala Val Gln Xaa Arg Arg
      165          170          175

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Leu Ile Ala Ile Cys Asp Val Ser Val Pro Leu Val Phe Leu Xaa Arg  
 180 185 190  
 His His Arg Lys Met Glu Asp His Thr Ala Val Arg Arg Arg Leu Lys  
 195 200 205  
 Pro Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 210 215 220  
 Xaa Leu Tyr Met Val Ser Ala Leu Ala Arg His Phe Ser Met Thr Phe  
 225 230 235 240  
 Xaa Ser Pro Ser Asp Leu Thr Ile Leu Ala Ile Ser Ala Thr Leu Met  
 245 250 255  
 Ala Val Tyr Thr Ser Phe Pro Ser Ile Val Met Val Met Arg Asn Gln  
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 275 280 285

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 ggagtcctta taaattctca tgattctggt aagtagccac tttctcctac tcaggccgat 180  
 catgttggaac ataagtctgt ttccactttc ccagagcagt gggttggttt actatcttaa 240  
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 tttgtttttt gctagtgtct ttcaagatca ctttttattt ctcagctctt gttggctgga 420  
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Met Asp Trp Val Lys Lys Arg Lys Ile Ala Ser Ile Asp Leu Ile Leu  
35 40 45  
Thr Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Leu Leu  
50 55 60  
Asp Cys Phe Ile Leu Val Leu Tyr Pro Asp Val Tyr Ala Thr Gly Lys  
65 70 75 80  
Glu Met Arg Ile Ile Asp Phe Phe Trp Thr Leu Thr Asn His Leu Ser  
85 90 95  
Ile Trp Phe Ala Thr Cys Leu Ser Ile Tyr Tyr Phe Phe Lys Ile Gly  
100 105 110  
Asn Phe Phe His Pro Leu Phe Leu Trp Met Lys Trp Arg Ile Asp Arg  
115 120 125  
Val Ile Ser Trp Ile Leu Leu Gly Cys Val Val Leu Ser Val Phe Ile  
130 135 140  
Ser Leu Pro Ala Thr Glu Asn Leu Asn Ala Asp Phe Arg Phe Cys Val  
145 150 155 160  
Lys Ala Lys Arg Lys Thr Asn Leu Thr Trp Ser Cys Arg Val Asn Lys  
165 170 175  
Thr Gln His Ala Ser Thr Lys Leu Phe Leu Asn Leu Ala Thr Leu Leu  
180 185 190  
Pro Phe Cys Val Cys Leu Met Ser Phe Phe Leu Leu Ile Leu Ser Leu  
195 200 205  
Arg Arg His Ile Arg Arg Met Gln Leu Ser Ala Thr Gly Cys Arg Asp  
210 215 220  
Pro Ser Thr Glu Ala His Val Arg Ala Leu Lys Ala Val Ile Ser Phe  
225 230 235 240  
Leu Leu Leu Phe Ile Ala Tyr Tyr Leu Ser Phe Leu Ile Ala Thr Ser  
245 250 255  
Ser Tyr Phe Met Pro Glu Thr Glu Leu Ala Val Ile Phe Gly Glu Ser  
260 265 270  
Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly  
275 280 285  
Asn Asn Lys Leu Arg His Ala Ser Leu Lys Val Ile Trp Lys Val Met  
290 295 300  
Ser Ile Leu Lys Gly Arg Lys Phe Gln Gln His Lys Gln Ile  
305 310 315

<210> 14  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R07 (hGR07)

<400> 14  
 atggcagata aagtgcagac tacttttattg ttcttagcag ttggagagtt ttcagtgggg 60  
 atcttaggga atgcattcat tggattggta aactgcatgg actgggtcaa gaagaggaaa 120  
 attgcctcca ttgattttaat cctcacaagt ctggccatat ccagaatttg tctattgtgc 180  
 gtaatactat tagattgttt tatattgggtg ctatatccag atgtctatgc cactggtaaa 240  
 gaaatgagaa tcattgactt cttctggaca ctaaccaatc atttaagtat ctggtttgca 300  
 acctgcctca gcatttacta tttcttcaag ataggttaatt tctttcacc ctttttcctc 360  
 tggatgaagt ggagaattga caggggtgatt tcctggattc tactggggtg cgtgggttctc 420  
 tctgtgttta ttagccttcc agccactgag aatttgaacg ctgatttcag gttttgtgtg 480  
 aaggcaaaga ggaaaacaaa cttaacttgg agttgcagag taaataaaaac tcaacatgct 540  
 tctaccaagt tattttctcaa cctggcaacg ctgctcccct tttgtgtgtg cctaattgtcc 600  
 tttttcctct tgatcctctc cctgcgagga catatcaggc gaatgcagct cagtgccaca 660  
 ggggtgcagag accccagcac agaagcccat gtgagagccc tgaaagctgt catttccttc 720  
 cttctcctct ttattgccta ctatttgtcc tttctcattg ccacctccag ctactttatg 780  
 ccagagacgg aattagctgt gatttttgggt gagtccatag ctctaatacta cccctcaagt 840  
 cattcattta tcttaatact ggggaacaat aaattaagac atgcatctct aaaggtgatt 900  
 tggaaagtaa tgtctattct aaaaggaaga aaattccaac aacataaaca aatctga 957

<210> 15  
 <211> 309  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R08 (hGR08)

<400> 15  
 Met Phe Ser Pro Ala Asp Asn Ile Phe Ile Ile Leu Ile Thr Gly Glu  
 1 5 10 15  
 Phe Ile Leu Gly Ile Leu Gly Asn Gly Tyr Ile Ala Leu Val Asn Trp  
 20 25 30  
 Ile Asp Trp Ile Lys Lys Lys Lys Ile Ser Thr Val Asp Tyr Ile Leu  
 35 40 45  
 Thr Asn Leu Val Ile Ala Arg Ile Cys Leu Ile Ser Val Met Val Val  
 50 55 60  
 Asn Gly Ile Val Ile Val Leu Asn Pro Asp Val Tyr Thr Lys Asn Lys  
 65 70 75 80  
 Gln Gln Ile Val Ile Phe Thr Phe Trp Thr Phe Ala Asn Tyr Leu Asn  
 85 90 95  
 Met Trp Ile Thr Thr Cys Leu Asn Val Phe Tyr Phe Leu Lys Ile Ala  
 100 105 110  
 Ser Ser Ser His Pro Leu Phe Leu Trp Leu Lys Trp Lys Ile Asp Met  
 115 120 125



Val Val His Trp Ile Leu Leu Gly Cys Phe Ala Ile Ser Leu Leu Val  
 130 135 140  
 Ser Leu Ile Ala Ala Ile Val Leu Ser Cys Asp Tyr Arg Phe His Ala  
 145 150 155 160  
 Ile Ala Lys His Lys Arg Asn Ile Thr Glu Met Phe His Val Ser Lys  
 165 170 175  
 Ile Pro Tyr Phe Glu Pro Leu Thr Leu Phe Asn Leu Phe Ala Ile Val  
 180 185 190  
 Pro Phe Ile Val Ser Leu Ile Ser Phe Phe Leu Leu Val Arg Ser Leu  
 195 200 205  
 Trp Arg His Thr Lys Gln Ile Lys Leu Tyr Ala Thr Gly Ser Arg Asp  
 210 215 220  
 Pro Ser Thr Glu Val His Val Arg Ala Ile Lys Thr Met Thr Ser Phe  
 225 230 235 240  
 Ile Phe Phe Phe Phe Leu Tyr Tyr Ile Ser Ser Ile Leu Met Thr Phe  
 245 250 255  
 Ser Tyr Leu Met Thr Lys Tyr Lys Leu Ala Val Glu Phe Gly Glu Ile  
 260 265 270  
 Ala Ala Ile Leu Tyr Pro Leu Gly His Ser Leu Ile Leu Ile Val Leu  
 275 280 285  
 Asn Asn Lys Leu Arg Gln Thr Phe Val Arg Met Leu Thr Cys Arg Lys  
 290 295 300  
 Ile Ala Cys Met Ile  
 305

<210> 16  
 <211> 930  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R08 (hGR08)

<400> 16  
 atgttcagtc ctgcagataa catctttata atcctaataa ctggagaatt catactagga 60  
 atattgggga atggatacat tgcactagtc aactggattg actggattaa gaagaaaaag 120  
 atttccacag ttgactacat ccttaccat ttagttatcg ccagaatttg tttgatcagt 180  
 gtaatgggtg taaatggcat tgtaatagta ctgaaccag atgtttatac aaaaaataaa 240  
 caacagatag tcatTTTTTt cttctggaca tttgccaaact acttaaatat gtggattacc 300  
 acctgcctta atgtcttcta ttttctgaag atagccagtt cctctcatcc actttttctc 360  
 tggctgaagt ggaaaattga tatggtggtg cactggatcc tgctgggatg ctttgccatt 420  
 tccttggttg tcagccttat agcagcaata gtactgagtt gtgattatag gtttcatgca 480  
 attgccaaac ataaaagaaa cattactgaa atgttccatg tgagtaaaat accatacttt 540  
 gaacccttga ctctctttaa cctgtttgca attgtcccat ttattgtgtc actgatatac 600  
 tttttccttt tagtaagatc tttatggaga cataccaagc aaataaaaact ctatgctacc 660  
 ggcagtagag accccagcac agaagttcat gtgagagcca ttaaaaactat gacttcattt 720  
 atcttctttt ttttcttata ctatatTTTt tctattttga tgacctttag ctatcttatg 780  
 acaaaataca agttagctgt ggagtttTga gagattgcag caattctcta ccccttgggt 840  
 cactcactta ttttaattgt tttaaataat aaactgaggc agacatttgt cagaatgctg 900

acatgtagaa aaattgcctg catgatatga

930

<210> 17

<211> 312

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R09 (hGR09)

<400> 17

Met Pro Ser Ala Ile Glu Ala Ile Tyr Ile Ile Leu Ile Ala Gly Glu  
1 5 10 15  
Leu Thr Ile Gly Ile Trp Gly Asn Gly Phe Ile Val Leu Val Asn Cys  
20 25 30  
Ile Asp Trp Leu Lys Arg Arg Asp Ile Ser Leu Ile Asp Ile Ile Leu  
35 40 45  
Ile Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Ser Leu  
50 55 60  
Asp Gly Phe Phe Met Leu Leu Phe Pro Gly Thr Tyr Gly Asn Ser Val  
65 70 75 80  
Leu Val Ser Ile Val Asn Val Val Trp Thr Phe Ala Asn Asn Ser Ser  
85 90 95  
Leu Trp Phe Thr Ser Cys Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala  
100 105 110  
Asn Ile Ser His Pro Phe Phe Phe Trp Leu Lys Leu Lys Ile Asn Lys  
115 120 125  
Val Met Leu Ala Ile Leu Leu Gly Ser Phe Leu Ile Ser Leu Ile Ile  
130 135 140  
Ser Val Pro Lys Asn Asp Asp Met Trp Tyr His Leu Phe Lys Val Ser  
145 150 155 160  
His Glu Glu Asn Ile Thr Trp Lys Phe Lys Val Ser Lys Ile Pro Gly  
165 170 175  
Thr Phe Lys Gln Leu Thr Leu Asn Leu Gly Val Met Val Pro Phe Ile  
180 185 190  
Leu Cys Leu Ile Ser Phe Phe Leu Leu Leu Phe Ser Leu Val Arg His  
195 200 205  
Thr Lys Gln Ile Arg Leu His Ala Thr Gly Phe Arg Asp Pro Ser Thr  
210 215 220  
Glu Ala His Met Arg Ala Ile Lys Ala Val Ile Ile Phe Leu Leu Leu  
225 230 235 240  
Leu Ile Val Tyr Tyr Pro Val Phe Leu Val Met Thr Ser Ser Ala Leu  
245 250 255

Ile Pro Gln Gly Lys Leu Val Leu Met Ile Gly Asp Ile Val Thr Val  
260 265 270

Ile Phe Pro Ser Ser His Ser Phe Ile Leu Ile Met Gly Asn Ser Lys  
275 280 285

Leu Arg Glu Ala Phe Leu Lys Met Leu Arg Phe Val Lys Cys Phe Leu  
290 295 300

Arg Arg Arg Lys Pro Phe Val Pro  
305 310

<210> 18  
<211> 939  
<212> DNA  
<213> Homo sapiens

<220>  
<223> human T2R09 (hGR09)

<400> 18  
atgccaaagt caatagaggc aatatatatt attttaattg ctggtgaatt gaccataggg 60  
atgtggggaa atggattcat tgtactagtt aactgcattg actggctcaa aagaagagat 120  
atctccttga ttgacatcat cctgatcagc ttggccatct ccagaatctg tctgctgtgt 180  
gtaatatcat tagatggctt ctttatgctg ctctttccag gtacatatgg caatagcgtg 240  
ctagtaagca ttgtgaatgt tgtctggaca tttgccaata attcaagtct ctggtttact 300  
tcttgccctca gtatcttcta ttactcaag atagccaata tatcgacccc atttttcttc 360  
tggctgaagc taaagatcaa caaggatcat cttgcgattc ttctgggggtc ctttcttctc 420  
tctttaatta ttagtggtcc aaagaatgat gatatgtggt atcacctttt caaagtcagt 480  
catgaagaaa acattacttg gaaattcaaa gtgagtaaaa ttccagggtac tttcaaacag 540  
ttaaccctga acctgggggt gatgggtccc tttatccttt gcctgatctc atttttcttg 600  
ttacttttct ccctagttag acacaccaag cagattcgac tgcattgctac aggggttcaga 660  
gaccccgagta cagaggccca catgagggcc ataaaggcag tgatcatctt tctgctctc 720  
ctcatcgtgt actaccagc ctttcttggt atgacctcta gcgctctgat tcttcaggga 780  
aaattagtggt tgatgattgg tgacatagta actgtcattt tcccatcaag ccattcattc 840  
attctaatta tgggaaatag caagttgagg gaagcttttc tgaagatggt aagatttggt 900  
aagtgtttcc ttagaagaag aaagcctttt gttccatag 939

<210> 19  
<211> 307  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human T2R10 (hGR10)

<400> 19  
Met Leu Arg Val Val Glu Gly Ile Phe Ile Phe Val Val Val Ser Glu  
1 5 10 15  
Ser Val Phe Gly Val Leu Gly Asn Gly Phe Ile Gly Leu Val Asn Cys  
20 25 30  
Ile Asp Cys Ala Lys Asn Lys Leu Ser Thr Ile Gly Phe Ile Leu Thr  
35 40 45  
Gly Leu Ala Ile Ser Arg Ile Phe Leu Ile Trp Ile Ile Ile Thr Asp  
50 55 60

Gly Phe Ile Gln Ile Phe Ser Pro Asn Ile Tyr Ala Ser Gly Asn Leu  
 65 70 75 80  
 Ile Glu Tyr Ile Ser Tyr Phe Trp Val Ile Gly Asn Gln Ser Ser Met  
 85 90 95  
 Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala Asn  
 100 105 110  
 Phe Ser Asn Tyr Ile Phe Leu Trp Leu Lys Ser Arg Thr Asn Met Val  
 115 120 125  
 Leu Pro Phe Met Ile Val Phe Leu Leu Ile Ser Ser Leu Leu Asn Phe  
 130 135 140  
 Ala Tyr Ile Ala Lys Ile Leu Asn Asp Tyr Lys Thr Lys Asn Asp Thr  
 145 150 155 160  
 Val Trp Asp Leu Asn Met Tyr Lys Ser Glu Tyr Phe Ile Lys Gln Ile  
 165 170 175  
 Leu Leu Asn Leu Gly Val Ile Phe Phe Phe Thr Leu Ser Leu Ile Thr  
 180 185 190  
 Cys Ile Phe Leu Ile Ile Ser Leu Trp Arg His Asn Arg Gln Met Gln  
 195 200 205  
 Ser Asn Val Thr Gly Leu Arg Asp Ser Asn Thr Glu Ala His Val Lys  
 210 215 220  
 Ala Met Lys Val Leu Ile Ser Phe Ile Ile Leu Phe Ile Leu Tyr Phe  
 225 230 235 240  
 Ile Gly Met Ala Ile Glu Ile Ser Cys Phe Thr Val Arg Glu Asn Lys  
 245 250 255  
 Leu Leu Leu Met Phe Gly Met Thr Thr Thr Ala Ile Tyr Pro Trp Gly  
 260 265 270  
 His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Ala Ser  
 275 280 285  
 Leu Arg Val Leu Gln Gln Leu Lys Cys Cys Glu Lys Arg Lys Asn Leu  
 290 295 300  
 Arg Val Thr  
 305

<210> 20

<211> 924

<212> DNA

<213> Homo sapiens

<220>

<223> human T2R10 (hGR10)

<400> 20

atgctacgtg tagtggaagg catcttcatt tttgtttag ttagtgagtc agtgtttggg 60  
 gttttgggga atggatttat tggacttgta aactgcattg actgtgccaa gaataagtta 120  
 tctacgattg gctttattct caccggctta gctatttcaa gaatttttct gatatggata 180

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ataattacag atggatttat acagatatcc tctccaaata tatatgcctc cggtaaccta 240
attgaatata ttagttactt ttgggtaatt ggtaatcaat caagtatgtg gtttgccacc 300
agcctcagca tcttctatct cctgaagata gcaaattttt ccaactacat atttctctgg 360
ttgaagagca gaacaaatat ggttcttccc ttcattgatag tattcttact tatttcacg 420
ttacttaatt ttgcatacat tgcgaagatt cttaatgatt ataaaacgaa gaatgacaca 480
gtctgggac tcaacatgta taaaagtga tactttatta aacagatttt gctaaatctg 540
ggagtcattt tcttctttac actatcccta attacatgta tttttttaat catttcctt 600
tgagagacaca acaggcagat gcaatcgaat gtgacaggat tgagagactc caacacagaa 660
gctcatgtga aggcaatgaa agttttgata tctttcatca tcctctttat cttgtatttt 720
ataggcatgg ccatagaaat atcatgtttt actgtgagag aaaacaaact gctgcttatg 780
tttggaatga caaccacagc catctatccc tggggtcact catttatctt aattctagga 840
aacagcaagc taaagcaagc ctctttgagg gtactgcagc aattgaagtg ctgtgagaaa 900
aggaaaaatc tcagagtcac atag                                     924

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<210> 21
<211> 245
<212> PRT
<213> Homo sapiens

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<220>
<223> human T2R11 (hGR11)

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<220>
<221> MOD_RES
<222> (1)..(245)
<223> Xaa = any amino acid

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<400> 21
Met Ala Asn Met Leu Lys Asn Met Leu Thr Met Ile Ser Ala Ile Asp
 1             5             10            15
Phe Ile Met Gly Ile Gln Arg Ser Arg Val Met Val Leu Val His Cys
      20             25             30
Ile Asp Trp Ile Arg Arg Trp Lys Leu Ser Leu Ile Asp Phe Ile Leu
      35             40             45
Thr Cys Trp Ala Ile Ser Arg Ile Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      50             55             60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      65             70             75             80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Leu Cys Thr Xaa Phe
      85             90             95
Ala Thr Cys Leu Ala Val Phe Tyr Phe Leu Lys Ile Val Asn Phe Ser
      100            105            110
Tyr Leu Phe Tyr Phe Trp Leu Lys Trp Arg Ile Asn Lys Val Ala Phe
      115            120            125
Ile Leu Pro Leu Val Ser Ala Phe Ser Val Tyr Gln Leu Ser Phe Asp
      130            135            140
Val His Phe Xaa Cys Leu Leu Val Ser Cys Pro Lys Lys Tyr Glu Arg
      145            150            155            160
His Met Thr Gly Leu Leu Asn Val Ser Asn Asn Lys Asn Val Asn Asn
      165            170            175

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Ile Ile Ile Phe Phe Ile Gly Ser Leu Ser Ser Phe Ser Ile Ser Ser  
                   180                                  185                                  190  
 Ile Phe Phe Leu Leu Leu Leu Leu Ser Ser Xaa Arg His Met Lys His  
                   195                                  200                                  205  
 Ile Arg Phe Asn Phe Arg Asp Cys Arg Thr Pro Val Tyr Gly Pro Ile  
                   210                                  215                                  220  
 Ser Glu Pro Arg Lys Arg Phe Ser Phe Phe Val Leu Leu Leu Tyr Lys  
                   225                                  230                                  235                                  240  
 Asn Leu Pro Phe Ser  
                                   245

<210> 22  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R12 (hGR12)

<220>  
 <221> MOD\_RES  
 <222> (1)..(315)  
 <223> Xaa = any amino acid

<400> 22  
 Met Ser Ser Ile Trp Glu Thr Leu Phe Ile Arg Ile Leu Val Val Xaa  
   1                  5                                  10                                  15  
 Phe Ile Met Gly Thr Val Gly Asn Xaa Phe Ile Val Leu Val Asn Ile  
                   20                                  25                                  30  
 Ile Asp Xaa Ile Arg Asn Xaa Lys Val Ser Leu Ile Asp Phe Ile Leu  
                   35                                  40                                  45  
 Asn Cys Leu Ala Ile Ser Arg Ile Cys Phe Leu Xaa Ile Thr Ile Leu  
                   50                                  55                                  60  
 Ala Thr Ser Phe Asn Ile Gly Tyr Glu Lys Met Pro Asp Ser Lys Asn  
   65                                  70                                  75                                  80  
 Leu Ala Val Ser Phe Asp Ile Leu Trp Thr Gly Ser Ser Tyr Phe Cys  
                   85                                  90                                  95  
 Leu Ser Cys Thr Thr Cys Leu Ser Val Phe Tyr Phe Leu Lys Val Ala  
                   100                                  105                                  110  
 Asn Phe Ser Asn Pro Ile Phe Leu Trp Met Lys Trp Lys Ile His Lys  
                   115                                  120                                  125  
 Val Leu Leu Phe Ile Val Leu Glu Ala Thr Ile Ser Phe Cys Thr Thr  
                   130                                  135                                  140  
 Ser Ile Leu Lys Glu Ile Ile Ile Asn Ser Leu Ile Xaa Glu Arg Val  
   145                                  150                                  155                                  160

Thr Ile Lys Gly Asn Leu Thr Phe Asn Tyr Met Asp Thr Met His Asp  
 165 170 175  
 Phe Thr Ser Leu Phe Leu Leu Gln Met Met Phe Ile Leu Pro Phe Val  
 180 185 190  
 Glu Thr Leu Ala Ser Ile Leu Leu Leu Ile Leu Ser Leu Trp Ser His  
 195 200 205  
 Thr Arg Gln Met Lys Leu His Gly Ile Tyr Ser Arg Asp Pro Ser Thr  
 210 215 220  
 Glu Ala His Val Lys Pro Ile Lys Ala Ile Ile Ser Phe Leu Leu Leu  
 225 230 235 240  
 Phe Ile Val His Tyr Phe Ile Ser Ile Ile Leu Thr Leu Ala Cys Pro  
 245 250 255  
 Leu Leu Asp Phe Val Ala Ala Arg Thr Phe Ser Ser Val Leu Val Phe  
 260 265 270  
 Phe His Pro Ser Gly His Ser Phe Leu Leu Ile Leu Arg Asp Ser Lys  
 275 280 285  
 Leu Lys Gln Ala Ser Leu Cys Val Leu Lys Lys Met Lys Tyr Ala Lys  
 290 295 300  
 Lys Asp Ile Ile Ser His Phe Tyr Lys His Ala  
 305 310 315

<210> 23  
 <211> 948  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R12 (hGR12)

<400> 23  
 atgtcaagca tttgggagac actgtttata agaattcttg tagtgtaatt cataatgggg 60  
 actgtgggaa attgattcat tgtattgggt aatatcattg actgaatcag gaactgaaag 120  
 gtctccctga ttgattttat tctcaactgc ttggccatct ccaggatatg tttcctgtag 180  
 ataacaattt tagctacctc tttcaatata ggctatgaga aaatgcctga ttctaagaat 240  
 cttgcagtaa gttttgacat tctctggaca ggatccagct atttctgcct gtcctgtacc 300  
 acttgccctca gtgtcttcta tttcctcaag gttagccaact tctccaatcc cattttcctc 360  
 tggatgaaat ggaaaattca caaggtgctt ctctttattg tactagaggc aacgatctct 420  
 ttctgcacaa ctccattct gaaggaaata ataattaata gtttaatcta agaacgggta 480  
 acaataaaaag gcaacttgac atttaattat atggatacca tgcattgatt cacttctctg 540  
 tttctccttc agatgatgtt catccttctt tttgtggaaa cactggcttc cattcttctc 600  
 ttaatcctct ccttatggag ccacaccagg cagatgaagc tacatgggtat ttattccagg 660  
 gatcccagca cagaagccca tgtaaaacct ataaaagcta taatttcatt tctactcctc 720  
 tttattgtgc attatttcat cagtatcata ctaacattgg cctgtcctct tctagacttc 780  
 gttgcggaag ggacttttag tagtgtgtct gtatttttcc atccatctgg ccattcattt 840  
 cttctaattt tacgggacag caaactgaag caagcttctc tctgtgtcct gaagaagatg 900  
 aagtatgcca aaaaggacat aatctctcat ttttataaac atgcctga 948

<210> 24  
 <211> 303  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R13 (hGR13)

<400> 24  
 Met Glu Ser Ala Leu Pro Ser Ile Phe Thr Leu Val Ile Ile Ala Glu  
 1 5 10 15  
 Phe Ile Ile Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ile Asn Cys  
 20 25 30  
 Ile Asp Trp Val Ser Lys Arg Glu Leu Ser Ser Val Asp Lys Leu Leu  
 35 40 45  
 Ile Ile Leu Ala Ile Ser Arg Ile Gly Leu Ile Trp Glu Ile Leu Val  
 50 55 60  
 Ser Trp Phe Leu Ala Leu His Tyr Leu Ala Ile Phe Val Ser Gly Thr  
 65 70 75 80  
 Gly Leu Arg Ile Met Ile Phe Ser Trp Ile Val Ser Asn His Phe Asn  
 85 90 95  
 Leu Trp Leu Ala Thr Ile Phe Ser Ile Phe Tyr Leu Leu Lys Ile Ala  
 100 105 110  
 Ser Phe Ser Ser Pro Ala Phe Leu Tyr Leu Lys Trp Arg Val Asn Lys  
 115 120 125  
 Val Ile Leu Met Ile Leu Leu Gly Thr Leu Val Phe Leu Phe Leu Asn  
 130 135 140  
 Leu Ile Gln Ile Asn Met His Ile Lys Asp Trp Leu Asp Arg Tyr Glu  
 145 150 155 160  
 Arg Asn Thr Thr Trp Asn Phe Ser Met Ser Asp Phe Glu Thr Phe Ser  
 165 170 175  
 Val Ser Val Lys Phe Thr Met Thr Met Phe Ser Leu Thr Pro Phe Thr  
 180 185 190  
 Val Ala Phe Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Gln Lys His  
 195 200 205  
 Leu Gln Lys Met Gln Leu Asn Tyr Lys Gly His Arg Asp Pro Arg Thr  
 210 215 220  
 Lys Val His Thr Asn Ala Leu Lys Ile Val Ile Ser Phe Leu Leu Phe  
 225 230 235 240  
 Tyr Ala Ser Phe Phe Leu Cys Val Leu Ile Ser Trp Ile Ser Glu Leu  
 245 250 255  
 Tyr Gln Asn Thr Val Ile Tyr Met Leu Cys Glu Thr Ile Gly Val Phe  
 260 265 270



Ser Pro Ser Ser His Ser Phe Leu Leu Ile Leu Gly Asn Ala Lys Leu  
 275 280 285

Arg Gln Ala Phe Leu Leu Val Ala Ala Lys Val Trp Ala Lys Arg  
 290 295 300

<210> 25  
 <211> 912  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R13 (hGR13)

<400> 25  
 atggaaagtg ccctgccgag tatcttcact cttgtaataa ttgcagaatt cataattggg 60  
 aatttgagca atggatttat agtactgac aactgcattg actgggtcag taaaagagag 120  
 ctgtcctcag tcgataaact cctcattatc ttggcaatct ccagaattgg gctgatctgg 180  
 gaaatattag taagttgggt tttagctctg cattatctag ccatatttgt gtctggaaca 240  
 ggattaagaa ttatgatttt tagctggata gtttctaata acttcaatct ctggcttgct 300  
 acaatcttca gcatctttta tttgctcaaa atagcgagtt tctctagccc tgcttttctc 360  
 tatttgaagt ggagagttaa caaagtgatt ctgatgatac tgctaggaac cttggtcttc 420  
 ttatttttaa atctgataca aataaacatg catataaaaag actggctgga ccgatatgaa 480  
 agaaacacaa cttggaattt cagtatgagt gactttgaaa cattttcagt gtcggtcaaa 540  
 ttcactatga ctatgttcag tctaacacca tttactgtgg ccttcacatc ttttctcctg 600  
 ttaattttct ccctgcagaa acatctccag aaaatgcaac tcaattacaa aggacacaga 660  
 gaccccagga ccaaggtcca taaaaatgcc ttgaaaattg tgatctcatt ccttttattc 720  
 tatgctagtt tctttctatg tgttctcata tcatggattt ctgagctgta tcagaacaca 780  
 gtgatctaca tgctttgtga gacgattgga gtcttctctc cttcaagcca ctcctttctt 840  
 ctgattctag gaaacgctaa gttaagacag gcctttcttt tggtggcagc taagggtatgg 900  
 gctaaacgat ga 912

<210> 26  
 <211> 317  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R14 (hGR14)

<400> 26  
 Met Gly Gly Val Ile Lys Ser Ile Phe Thr Phe Val Leu Ile Val Glu  
 1 5 10 15  
 Phe Ile Ile Gly Asn Leu Gly Asn Ser Phe Ile Ala Leu Val Asn Cys  
 20 25 30  
 Ile Asp Trp Val Lys Gly Arg Lys Ile Ser Ser Val Asp Arg Ile Leu  
 35 40 45  
 Thr Ala Leu Ala Ile Ser Arg Ile Ser Leu Val Trp Leu Ile Phe Gly  
 50 55 60  
 Ser Trp Cys Val Ser Val Phe Phe Pro Ala Leu Phe Ala Thr Glu Lys  
 65 70 75 80  
 Met Phe Arg Met Leu Thr Asn Ile Trp Thr Val Ile Asn His Phe Ser  
 85 90 95

Val Trp Leu Ala Thr Gly Leu Gly Thr Phe Tyr Phe Leu Lys Ile Ala  
 100 105 110  
 Asn Phe Ser Asn Ser Ile Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys  
 115 120 125  
 Val Val Leu Val Leu Leu Leu Val Thr Ser Val Phe Leu Phe Leu Asn  
 130 135 140  
 Ile Ala Leu Ile Asn Ile His Ile Asn Ala Ser Ile Asn Gly Tyr Arg  
 145 150 155 160  
 Arg Asn Lys Thr Cys Ser Ser Asp Ser Ser Asn Phe Thr Arg Phe Ser  
 165 170 175  
 Ser Leu Ile Val Leu Thr Ser Thr Val Phe Ile Phe Ile Pro Phe Thr  
 180 185 190  
 Leu Ser Leu Ala Met Phe Leu Leu Leu Ile Phe Ser Met Trp Lys His  
 195 200 205  
 Arg Lys Lys Met Gln His Thr Val Lys Ile Ser Gly Asp Ala Ser Thr  
 210 215 220  
 Lys Ala His Arg Gly Val Lys Ser Val Ile Thr Phe Phe Leu Leu Tyr  
 225 230 235 240  
 Ala Ile Phe Ser Leu Ser Phe Phe Ile Ser Val Trp Thr Ser Glu Arg  
 245 250 255  
 Leu Glu Glu Asn Leu Ile Ile Leu Ser Gln Val Met Gly Met Ala Tyr  
 260 265 270  
 Pro Ser Cys His Ser Cys Val Leu Ile Leu Gly Asn Lys Lys Leu Arg  
 275 280 285  
 Gln Ala Ser Leu Ser Val Leu Leu Trp Leu Arg Tyr Met Phe Lys Asp  
 290 295 300  
 Gly Glu Pro Ser Gly His Lys Glu Phe Arg Glu Ser Ser  
 305 310 315

<210> 27  
 <211> 954  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> huamn T2R14 (hGR14)

<400> 27  
 atggggtggtg tcataaagag catattttaca ttcgtttttaa ttgtggaatt tataattgga 60  
 aatttaggaa atagtttcat agcactggtg aactgtattg actgggtcaa gggaagaaag 120  
 atctcttcgg ttgatcggat cctcactgct ttggcaatct ctggaattag cctggttttg 180  
 ttaatatctg gaagctggtg tgtgtctgtg tttttccag ctttatttgc cactgaaaaa 240  
 atgttcagaa tgcttactaa tatctggaca gtgatcaatc attttagtgt ctggttagct 300  
 acaggcctcg gtacttttta ttttctcaag atagccaatt tttctaactc tattttttctc 360  
 tacctaaagt ggagggttaa aaagggtggtt ttggtgctgc ttcttgtgac ttcggtcttc 420  
 ttgtttttta atattgcact gataaacatc catataaatg ccagtatcaa tggatacaga 480  
 agaaacaaga cttgcagttc tgattcaagt aactttaacac gattttccag tcttattgta 540

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ttaaccagca ctgtgttcat tttcataccc tttactttgt ccctggcaat gtttcttctc 600
ctcatcttct ccatgtggaa acatcgcaag aagatgcagc acactgtcaa aatatccgga 660
gacgccagca ccaaagccca cagaggagtt aaaagtgtga tcactttctt cctactctat 720
gccattttct ctctgtcttt tttcatatca gtttggacct ctgaaagggt ggaggaaaat 780
ctaattattc tttcccaggt gatgggaatg gcttatcctt catgtcactc atgtgttctg 840
attcttggaa acaagaagct gagacaggcc tctctgtcag tgctactgtg gctgaggtag 900
atgttcaaag atggggagcc ctcagggtcac aaagaattta gagaatcatc ttga      954

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<210> 28

<211> 300

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R15 (hGR15)

<220>

<221> MOD\_RES

<222> (257)

<223> Xaa = any amino acid

<400> 28

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Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Val Thr
 1             5             10             15

Phe Val Leu Gly Asn Phe Ala Asn Gly Phe Ile Val Leu Val Asn Ser
      20             25             30

Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
      35             40             45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
      50             55             60

His Trp Tyr Ala Thr Val Leu Asn Pro Gly Ser Tyr Ser Leu Gly Val
      65             70             75             80

Arg Ile Thr Thr Ile Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
      85             90             95

Trp Val Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala Asn
      100            105            110

Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Ile Lys Ser Val
      115            120            125

Ile Pro Val Ile Leu Leu Gly Ser Leu Leu Phe Leu Val Cys His Leu
      130            135            140

Val Val Val Asn Met Asp Glu Ser Met Trp Thr Lys Glu Tyr Glu Gly
      145            150            155            160

Asn Val Ser Trp Glu Ile Lys Leu Ser Asp Pro Thr His Leu Ser Asp
      165            170            175

Met Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
      180            185            190

Leu Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
      195            200            205

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Met Gln Phe His Gly Lys Gly Ser Pro Asp Ser Asn Thr Lys Val His  
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Phe Ala Val  
 225 230 235 240

Tyr Phe Leu Ser Leu Ile Thr Ser Ile Trp Asn Phe Arg Arg Arg Leu  
 245 250 255

Xaa Asn Glu Pro Val Leu Met Leu Ser Gln Thr Thr Ala Ile Ile Tyr  
 260 265 270

Pro Ser Phe His Ser Phe Ile Leu Ile Trp Gly Ser Lys Lys Leu Lys  
 275 280 285

Gln Thr Phe Leu Leu Ile Leu Cys Gln Ile Lys Cys  
 290 295 300

<210> 29  
 <211> 903  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R15 (hGR15)

<400> 29  
 atgataactt ttctacccat cattttttcc attctagtag tggttacatt tggtcttggg 60  
 aattttgcta atggcttcat agtggttgga aattccattg agtgggtcaa gagacaaaag 120  
 atctcctttg ctgaccaaatt tctcactgct ctggcagtct ccagagttgg ttggtctctgg 180  
 gtaataattat tacatttgga tgcaactggt ttgaatccag gttcatatag tttaggagta 240  
 agaattacta ctattaatgc ctgggctgta accaaccatt tcagcatctg ggttgctact 300  
 agcctcagca tatttttattt cctcaagatt gccaatcttct ccaactttat ttttcttcac 360  
 ttaaaaagga gaattaagag tgtcattcca gtgatactat tgggggtcttt gttatttttg 420  
 gtttgtcatc ttgttggtgt aaacatggat gagagtatgt ggacaaaaga atatgaagga 480  
 aacgtgagtt gggagatcaa attgagtgat ccgacgcacc tttcagatat gactgtaacc 540  
 acgcttgcaa acttaataacc ctttactctg tccctgttat cttttctgct cttaatctgt 600  
 tctttgtgta aacatctcaa gaagatgcag ttccatggca aaggatctcc agattccaac 660  
 accaaggctc acataaaaagc ttgcaaacg gtgacctcct tcctcttggt atttgctggt 720  
 tactttctgt ccctaattcac atcgatttgg aatttttagga ggaggctgta gaacgaacct 780  
 gtccatcatg tcagccaaac tactgcaatt atataccctt catttcattc attcatccta 840  
 atttggggaa gcaagaagct gaaacagacc tttcttttga ttttgtgtca gattaagtgc 900  
 tga 903

<210> 30  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R16 (hGR16)

<400> 30  
 Met Ile Pro Ile Gln Leu Thr Val Phe Phe Met Ile Ile Tyr Val Leu  
 1 5 10 15

Glu Ser Leu Thr Ile Ile Val Gln Ser Ser Leu Ile Val Ala Val Leu  
 20 25 30

Gly Arg Glu Trp Leu Gln Val Arg Arg Leu Met Pro Val Asp Met Ile  
                   35                                  40                                  45  
 Leu Ile Ser Leu Gly Ile Ser Arg Phe Cys Leu Gln Trp Ala Ser Met  
                   50                                  55                                  60  
 Leu Asn Asn Phe Cys Ser Tyr Phe Asn Leu Asn Tyr Val Leu Cys Asn  
                   65                                  70                                  75                                  80  
 Leu Thr Ile Thr Trp Glu Phe Phe Asn Ile Leu Thr Phe Trp Leu Asn  
                                   85                                  90                                  95  
 Ser Leu Leu Thr Val Phe Tyr Cys Ile Lys Val Ser Ser Phe Thr His  
                                   100                                  105                                  110  
 His Ile Phe Leu Trp Leu Arg Trp Arg Ile Leu Arg Leu Phe Pro Trp  
                   115                                  120                                  125  
 Ile Leu Leu Gly Ser Leu Met Ile Thr Cys Val Thr Ile Ile Pro Ser  
                   130                                  135                                  140  
 Ala Ile Gly Asn Tyr Ile Gln Ile Gln Leu Leu Thr Met Glu His Leu  
                   145                                  150                                  155                                  160  
 Pro Arg Asn Ser Thr Val Thr Asp Lys Leu Glu Asn Phe His Gln Tyr  
                                   165                                  170                                  175  
 Gln Phe Gln Ala His Thr Val Ala Leu Val Ile Pro Phe Ile Leu Phe  
                                   180                                  185                                  190  
 Leu Ala Ser Thr Ile Phe Leu Met Ala Ser Leu Thr Lys Gln Ile Gln  
                   195                                  200                                  205  
 His His Ser Thr Gly His Cys Asn Pro Ser Met Lys Ala Arg Phe Thr  
                   210                                  215                                  220  
 Ala Leu Arg Ser Leu Ala Val Leu Phe Ile Val Phe Thr Ser Tyr Phe  
                   225                                  230                                  235                                  240  
 Leu Thr Ile Leu Ile Thr Ile Ile Gly Thr Leu Phe Asp Lys Arg Cys  
                                   245                                  250                                  255  
 Trp Leu Trp Val Trp Glu Ala Phe Val Tyr Ala Phe Ile Leu Met His  
                                   260                                  265                                  270  
 Ser Thr Ser Leu Met Leu Ser Ser Pro Thr Leu Lys Arg Ile Leu Lys  
                   275                                  280                                  285  
 Gly Lys Cys  
                   290

<210> 31  
 <211> 876  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R16 (hGR16)

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<400> 31
atgataccca tccaactcac tgtcttcttc atgatcatct atgtgcttga gtccttgaca 60
attattgtgc agagcagcct aattgttgca gtgctgggca gagaatggct gcaagtcaga 120
aggctgatgc ctgtggacat gattctcatc agcctgggca tctctcgctt ctgtctacag 180
tgggcatcaa tgctgaacaa tttttgctcc tattttaatt tgaattatgt actttgcaac 240
ttaacaatca cctgggaatt ttttaatatc cttacattct ggtaaacag cttgcttacc 300
gtgttctact gcatcaaggc ctcttctttc acccatcaca tctttctctg gctgagggtg 360
agaattttga ggttggttcc ctggatatta ctgggttctc tgatgattac ttgtgtaaca 420
atcatccctt cagctattgg gaattacatt caaattcagt tactcaccat ggagcatcta 480
ccaagaaaca gcaactgtaac tgacaaactt gaaaattttc atcagtatca gttccaggct 540
catacagttg cattgggtat tcctttcatc ctgttcctgg cctccaccat ctttctcatg 600
gcatcactga ccaagcagat acaacatcat agcactggtc actgcaatcc aagcatgaaa 660
gcgcgcttca ctgccctgag gtcccttgcc gtcttattta ttgtgtttac ctcttacttt 720
ctaaccatac tcatcaccat tatagggtact ctatttgata agagatgttg gttatgggtc 780
tggaagctt ttgtctatgc tttcatctta atgcattcca cttcactgat gctgagcagc 840
cctacgttga aaaggattct aaagggaag tgctag 876

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<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

```

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<220>
<223> human T2R17 (hGR17)

<220>
<221> MOD_RES
<222> (1)..(330)
<223> Xaa = any amino acid

```

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<400> 32
Met Cys Ser Ala Xaa Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe
  1             5             10             15

Ala Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Ile Asn
      20             25             30

Val Asn Asp Trp Val Lys Thr Gln Lys Ile Ser Ser Thr Asp Gln Ile
      35             40             45

Val Thr Ala Leu Ala Phe Ser Arg Ile Gly Leu Leu Xaa Thr Leu Ile
      50             55             60

Ile Leu Leu His Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Ser
      65             70             75             80

Leu Glu Val Arg Ile Val Pro Ser Asn Val Ser Ala Ile Ile Asn His
      85             90             95

Phe Ser Ile Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Phe Lys
      100            105            110

Ile Ala Asn Phe Ser Asn Phe Ile Phe Leu His Leu Lys Lys Arg Ile
      115            120            125

Lys Ser Val Leu Leu Val Ile Leu Leu Gly Ser Leu Val Phe Leu Ile
      130            135            140

Cys Asn Leu Ala Val Val Thr Met Asp Asp Ser Val Trp Thr Lys Glu
      145            150            155            160

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Asp Ser Phe Ile Met Val Leu Ser Pro His Leu Tyr Thr Ile Arg Lys  
 65 70 75 80  
 Leu Val Lys Leu Phe Thr Ile Leu Trp Ala Leu Ile Asn Gln Leu Ser  
 85 90 95  
 Ile Xaa Phe Ala Thr Cys Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala  
 100 105 110  
 Asn Phe Ser His Ser Leu Phe Leu Trp Leu Lys Trp Arg Met Asn Gly  
 115 120 125  
 Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp  
 130 135 140  
 Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp  
 145 150 155 160  
 Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp  
 165 170 175  
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Tyr Val Ile Pro  
 180 185 190  
 Phe Leu Leu Thr Leu Thr Ser Leu Leu Leu Leu Phe Ile Ser Leu Val  
 195 200 205  
 Arg His Thr Lys Asn Leu Gln Leu Asn Ser Leu Gly Ser Arg Asp Ser  
 210 215 220  
 Ser Thr Glu Ala His Lys Arg Ala Met Lys Met Val Ile Ala Phe Leu  
 225 230 235 240  
 Leu Leu Phe Ile Ile Asn Phe Ile Ser Thr Leu Ile Gly Asp Trp Ile  
 245 250 255  
 Phe Leu Glu Val Glu Asn Tyr Gln Val Met Met Phe Ile Met Met Ile  
 260 265 270  
 Leu Leu Ala Phe Pro Ser Gly His Ser Phe Ile Ile Ile Leu Gly Asn  
 275 280 285  
 Asn Lys Leu Arg Gln Ser Ser Leu Arg Leu Leu Trp His Leu Lys Phe  
 290 295 300  
 Ser Leu Lys Lys Ala Lys Pro Leu Thr Ser  
 305 310

<210> 34  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R18 (hGR18)

<400> 34  
 atgttcggtg gaattaatat tttctttctg gtgggtggcaa caagaggact tgtcttagga 60  
 atgctgggaa acgggctcat tggactggta aactgcattg agtggggcaa gagttggaag 120  
 gtctcatcag ctgatttcac cctcaccagc ttggctatag tcagaatcat tcgactgtat 180



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ttaataactat ttgattcatt tataatggta ttgtccccc atctatatac catccgtaaa 240
ctagtaaaaac tgtttactat tctttgggca ttaattaatc agttaagtat ctagtttgcc 300
acctgcctaa gcattttcta cttgcttaag atagccaatt tctcccactc ccttttcctc 360
tggctgaagt ggagaatgaa cggaatgatt gttatgcttc ttatattgtc tttgttctta 420
ctgatttttg acagttagt gctagaaata tttattgata tctcactcaa tataatagat 480
aaaagtaatc tgactttata tttagatgaa agtaaaaactc tctatgataa actctctatt 540
ttaaaaaactc ttctcagctt gacatacggtt attccctttc ttctgactct gacctctttg 600
ctccttttat ttatatcctt agtgagacac accaagaatt tgcagctcaa ctctctgggc 660
tcaagggact ccagcacaga ggcccataaa agggccatga aaatgggtgat agccttcctc 720
ctccttttta ttattaactt tatttccact ttaataggag attggatctt ccttgaggta 780
gagaattatc aggtcatgat gtttattatg atgattttac ttgcctttcc ctcaggccac 840
tcatttatta taattttggg aaacaacaag ctaagacaga gctccttgag actactgtgg 900
catcttaaatt tctctctgaa aaaagcaaaa cctttaactt catag 945

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<210> 35  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R19 (hGR19)

<400> 35  
 Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu Ile Cys  
 1 5 10 15  
 Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys Met Arg  
 20 25 30  
 Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile Lys  
 35 40 45  
 Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile Tyr Phe  
 50 55 60  
 Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln Ser Lys  
 65 70 75 80  
 Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro Ser Phe  
 85 90 95  
 His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln Thr Phe  
 100 105 110  
 Leu Ser Val Leu Trp Gln Met Thr Cys  
 115 120

<210> 36  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R19 (hGR19)

<400> 36  
 ctgtaactac tctagcaaac ctcataccct ttactctgag cctaatatgt tttctgctgt 60  
 taatctgttc tctttgtaaa catctcaaga agatgaggct ccatagcaaa ggatctcaag 120  
 atcccagcac caaggtccat ataaaagctt tgcaaaactgt gacctccttc ctcatgttat 180

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ttgccattta ctttctgtgt ataatcacat caacttggaa tcttaggaca cagcagagca 240
aacttgtagt cctgctttgc caaactgttg caatcatgta tccttcattc cactcattca 300
tcctgattat gggaagtagg aagctaaaac agacctttct ttcagttttg tggcagatga 360
catgctgagt gaaagaagag aaaccctcaa ctccatagat tcacaagggg agcatcgtgg 420
gtcttctagc agaaaacaaa ctgatggtgt ctggaacatt ttatat 466

```

```

<210> 37
<211> 129
<212> PRT
<213> Homo sapiens

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```

<220>
<223> human T2R20 (hGR20)

```

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<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

```

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<400> 37
His Leu Xaa Arg Lys Ala Lys Ser Val Val Leu Val Ile Val Leu Gly
  1              5              10              15

Ser Leu Phe Phe Leu Val Cys Gln Leu Val Met Lys Asn Thr Tyr Ile
      20              25              30

Asn Val Trp Thr Glu Glu Cys Glu Gly Asn Val Thr Trp Lys Ile Lys
      35              40              45

Leu Arg Asn Ala Met His Leu Ser Asn Leu Thr Val Ala Met Leu Ala
      50              55              60

Asn Leu Ile Pro Phe Thr Leu Thr Val Ile Ser Phe Leu Leu Leu Ile
      65              70              75              80

Tyr Ser Leu Cys Lys His Leu Lys Lys Met Gln Leu His Gly Lys Gly
      85              90              95

Ser Gln Asp Pro Ser Thr Lys Ile His Ile Lys Ala Leu Gln Thr Val
      100              105              110

Thr Ser Phe Leu Val Leu Leu Ala Ile Tyr Phe Leu Cys Leu Ile Ile
      115              120              125

Ser

```

```

<210> 38
<211> 397
<212> DNA
<213> Homo sapiens

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<220>
<223> human T2R20 (hGR20)

```

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<220>
<221> modified_base
<222> (12)
<223> n = g, a, c or t

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<400> 38
ttcatcactt anaaaggaag gctaagagtg tagttctggt gatagtgttg gggctcttgt 60
tctttttggt ttgtcaactt gtgatgaaaa acacgtatat aaatgtgttg acagaagaat 120
gtgaaggaaa cgtaacttgg aagatcaaac tgaggaatgc aatgcacctt tccaacttga 180
ctgtagccat gctagcaaac ttgataccat tcaactctgac cgtgatatct tttctgctgt 240
taatctactc tctgtgtaaa catctgaaga agatgcagct ccatggcaaa ggatctcaag 300
atcccagcac caagatccac ataaaagctc tgcaaactgt gacctccttc ctcgtattac 360
ttgccattta ctttctgtgt ctaatcatat cctttttg 397

```

```

<210> 39
<211> 312
<212> PRT
<213> Homo sapiens

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<220>
<223> human T2R21 (hGR21)

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<220>
<221> MOD_RES
<222> (1)..(312)
<223> Xaa = any amino acid

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<400> 39
Met Pro Pro Gly Ile Gly Asn Thr Phe Leu Ile Val Met Met Gly Glu
  1             5             10             15

Phe Ile Ile Xaa Met Leu Gly Asn Gly Phe Ile Val Leu Val Asn Cys
      20             25             30

Ile Asp Trp Xaa Gly Val Lys Xaa Ser Tyr Xaa Thr Thr Ala Ser Ser
  35             40             45

Pro Ala Trp Leu Ser Pro Gln Ser Val Asn Phe Gly Xaa Tyr Tyr Leu
  50             55             60

Ile His Leu Xaa Gln His Tyr Gly His Ile Tyr Met Pro Ser Ile Asn
  65             70             75             80

Xaa Xaa Asn Leu Phe Ile Phe Phe Gly His Xaa Pro Ile Thr Xaa Leu
      85             90             95

Pro Gly Leu Leu Pro Xaa Cys Phe Leu Leu Leu Xaa Asn Thr Tyr Phe
  100            105            110

Ser His Pro Cys Phe Ile Trp Leu Arg Trp Arg Ile Ser Arg Thr Leu
  115            120            125

Leu Glu Leu Pro Leu Gly Ser Leu Leu Leu Leu Phe Phe Asn Leu Ala
  130            135            140

Leu Thr Gly Gly Leu Ser Asp Leu Trp Ile Asn Ile Tyr Thr Ile Tyr
  145            150            155            160

Glu Arg Asn Ser Thr Trp Ser Leu Asp Val Ser Lys Ile Leu Tyr Cys
      165            170            175

Ser Leu Trp Ile Leu Val Ser Leu Ile Tyr Leu Ile Ser Phe Leu Leu
  180            185            190

```

Ser Leu Ile Ser Leu Leu Leu Leu Ile Leu Ser Leu Met Arg His Ile  
 195 200 205  
 Arg Asn Leu Gln Leu Asn Thr Met Gly Pro Arg Asp Leu Arg Met Lys  
 210 215 220  
 Ala His Lys Arg Ala Met Lys Met Lys Met Lys Met Met Val Ser Phe  
 225 230 235 240  
 Leu Leu Phe Phe Leu Val His Phe Ser Ser Leu Leu Pro Thr Gly Trp  
 245 250 255  
 Ile Phe Leu Ile Gln Gln Lys Xaa Gln Ala Asn Phe Phe Val Leu Leu  
 260 265 270  
 Thr Ser Ile Ile Phe Pro Ser Ser His Ser Phe Val Leu Ile Leu Glu  
 275 280 285  
 Asn Cys Lys Leu Arg Gln Thr Ala Val Gly Pro Leu Trp His Leu Lys  
 290 295 300  
 Cys His Leu Lys Arg Val Lys Leu  
 305 310

<210> 40  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R22 (hGR22)

<220>  
 <221> MOD\_RES  
 <222> (1)..(90)  
 <223> Xaa = any amino acid

<400> 40  
 Met Ala Thr Glu Ser Asp Thr Asn Leu Leu Ile Leu Ala Ile Ala Glu  
 1 5 10 15  
 Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys  
 20 25 30  
 Ser Glu Xaa Ile Lys Asn Xaa Lys Val Phe Ser Ala Asp Phe Ile Leu  
 35 40 45  
 Thr Cys Leu Ala Ile Ser His Asn Gly Gln Leu Leu Val Ile Leu Phe  
 50 55 60  
 Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg  
 65 70 75 80  
 Leu Xaa Lys Asn Cys Ile Met Leu Trp Thr  
 85 90

<210> 41  
 <211> 656  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R22 (hGR22)

<220>  
 <221> modified\_base  
 <222> (1)..(656)  
 <223> n = g, a, c or t

<400> 41  
 tatagggacn gtgatgcttc gtacactctc caagaagaaa cactccgtga ggtatgtgag 60  
 actgcatncc ttagtagatc tnttgggata tatattcata atatagaaaa anaggcaaag 120  
 acttncctaa gtatatgaga ctctatccaa cagcagaagg ttctgatcaa gactggaagt 180  
 gcaatanaag caatgaagat aagtatcaga tatgaatgct cttctgcaat ggtctgattg 240  
 tnacattatt aatgatacan agtattaaaa acttggattt tnttgtctct ggagatggcc 300  
 accgaatcgg acacaaatct tctgattctg gcaatagcag aattcatcat cagcatgctg 360  
 gggaaatgtgt tcattggact ggtaaaactgc tctgaangga tcaagaacca naaggtcttc 420  
 tcagctgact tcattcctcac ctgcttggtc atctctcaca atggacaact gttggtgata 480  
 ctgttttgatt catttctagt gggacttgct tcacatctat ataccacata tagactanga 540  
 aaaaactgta ttatgctttg gacatgacta atcacttgac acactgcttc gcacgtgcta 600  
 gcatattcta ttcttagata gccacttcnc actccttgct tctgctgaag tgggat 656

<210> 42  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R23 (hGR23)

<220>  
 <221> MOD\_RES  
 <222> (1)..(72)  
 <223> Xaa = any amino acid

<400> 42  
 Val Ala Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Val  
 1 5 10 15  
 Asn Val Ile Asp Xaa Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln  
 20 25 30  
 Ile Leu Thr Ala Leu Val Val Ser Arg Ile Gly Xaa Thr Leu Xaa His  
 35 40 45  
 Ser Ile Pro Xaa Asp Ala Thr Arg Cys Xaa Ser Ala Leu Tyr Arg Xaa  
 50 55 60  
 Glu Val Arg Ile Val Ala Ser Asn  
 65 70

<210> 43  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens

<220>  
<223> human T2R23 (hGR23)

<220>  
<221> modified\_base  
<222> (1)..(589)  
<223> n = g, a, c or t

<400> 43  
agggttgagt cgtgcttatac ttcaacttaac ctagtatana antacagcat atagcaagga 60  
gagaatgtat atgaagagga gtgaatttga gtctgtttga gaataatgac cttttctatt 120  
tctataaaga cagttttgaa ttcattctatt agcatatgct ggtgcttgcc tgttgacact 180  
agtcaactgaa tttaaaggca gaaaatgtta ttgcacattt agtaatcaag tgttcacga 240  
agttaacatc tggatgttaa aggactcaga acaagtgtta ctaagcctgc atttttttat 300  
ctgttcaaac atgatgtgtt ntctgctcat catttcatca attctggtag agttgcattt 360  
gttcttgga atgtngccaa tggcttcata gctctagtaa atgtcattga ctgngttaac 420  
acacgaaaga tctcctcagc tgagcaaatt ctcactgctc tgggtggtctc cagaattggt 480  
nntactctgn gtcatagtat tccttgagat gcaactagat gttaattctgc tctatatagg 540  
ntagaagtaa gaattgttgc ttctaattgcc tgagctcgta cgaaccatt 589

<210> 44  
<211> 314  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human T2R24 (hGR24)

<400> 44  
Met Ala Thr Glu Leu Asp Lys Ile Phe Leu Ile Leu Ala Ile Ala Glu  
1 5 10 15  
Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys  
20 25 30  
Ser Glu Gly Ile Lys Asn Gln Lys Val Phe Ser Ala Asp Phe Ile Leu  
35 40 45  
Thr Cys Leu Ala Ile Ser Thr Ile Gly Gln Leu Leu Val Ile Leu Phe  
50 55 60  
Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg  
65 70 75 80  
Leu Gly Lys Thr Val Ile Met Leu Trp His Met Thr Asn His Leu Thr  
85 90 95  
Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala  
100 105 110  
His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly  
115 120 125  
Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp  
130 135 140  
Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp  
145 150 155 160

Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp  
 165 170 175  
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro  
 180 185 190  
 Phe Ser Leu Phe Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val  
 195 200 205  
 Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser  
 210 215 220  
 Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu  
 225 230 235 240  
 Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Gly Ile  
 245 250 255  
 Phe Phe Met Leu Trp Asn Asn Lys Tyr Ile Lys Phe Val Met Leu Ala  
 260 265 270  
 Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn  
 275 280 285  
 Ser Lys Leu Arg Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn  
 290 295 300  
 Tyr Thr Lys Thr Pro Asn Ala Leu Pro Leu  
 305 310

<210> 45  
 <211> 945  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <223> human T2R24 (hGR24)

<400> 45  
 atggccaccg aattggacaa aatctttctg attctggcaa tagcagaatt catcatcagc 60  
 atgctgggga atgtgttcat tggactggta aactgctctg aagggatcaa gaacccaaaag 120  
 gtcttctcag ctgacttcat cctcacctgc ttggctatct ccacaattgg acaactgttg 180  
 gtgatactgt ttgattcatt tctagtggga cttgcttcac atttatatac cacatataga 240  
 ctaggaaaaa ctgttattat gctttggcac atgactaatc acttgacaac ctggcttgcc 300  
 acctgcctaa gcattttcta tttctttaag atagccact tccccactc cttttcctc 360  
 tggctgaggt ggaggatgaa cggaatgatt gttatgcttc ttatattgtc tttgttctta 420  
 ctgatttttg acagtttagt gctagaaata tttattgata tctcactcaa tataatagat 480  
 aaaagtaatc tgactttata tttagatgaa agtaaaactc tctatgataa actctctatt 540  
 ttaaaaactc ttctcagctt aaccagtttt atcccccttt ctctgttcct gacctccttg 600  
 ctttttttat ttctgtcctt ggtgagacat actagaaatt tgaagctcag ttccttgggc 660  
 tctagagact ccagcacaga ggcccatagg agggccatga aaatggtgat gtctttcctt 720  
 ttcctcttca tagttcattt tttttcctta caagtggcca atgggatatt ttttatgttg 780  
 tggaacaaca agtacataaa gtttgatcat ttagccttaa atgcctttcc ctctgtgccac 840  
 tcatttattc tcattctggg aaacagcaag ctgcgcacaga cagctgtgag gctactgtgg 900  
 catcttagga actatacaaa aacaccaa atgctttacct tgttag 945

<210> 46  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R25 (hGR25)

<400> 46  
 Leu Ser Pro Phe Arg Met Leu Phe Ala Ile Tyr Phe Leu Cys Ile Ile  
   1                  5                  10                  15  
 Thr Ser Thr Trp Asn Pro Arg Thr Gln Gln Ser Asn Leu Val Phe Leu  
                   20                  25                  30  
 Leu Tyr Gln Thr Leu Ala Ile Met Tyr Pro Ser Phe His Ser Phe Ile  
           35                  40                  45  
 Leu Ile Met Arg Ser Arg Lys Leu Lys Gln Thr Ser Leu Ser Val Leu  
       50                  55                  60  
 Cys Gln Val Thr Cys Trp Val Lys  
   65                  70

<210> 47  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R26 (hGR26)

<220>  
 <221> MOD\_RES  
 <222> (20)  
 <223> Xaa = any amino acid

<400> 47  
 Met Pro Pro Gly Ile Gly Asn Thr Phe Leu Ile Val Met Met Gly Glu  
   1                  5                  10                  15  
 Phe Ile Ile Xaa Met Leu Gly Asn Gly Phe Ile Val Leu Val Asn Cys  
           20                  25                  30  
 Ile Asp Val Arg Ser Gln Met Ile Leu Leu Asp Asn Cys Ile Leu Thr  
       35                  40                  45  
 Ser Leu Ala Ile Ser Thr Ile Ser Gln Leu Trp Ile Ile Leu Leu Asp  
       50                  55                  60  
 Ser Phe Val Thr Ala Leu Trp Pro His Leu Tyr Ala Phe Asn Lys Leu  
       65                  70                  75                  80  
 Ile Lys Phe Ile His Ile Phe Trp Ala Leu Thr Asn His Leu Val Thr  
           85                  90                  95  
 Trp Leu Ala Cys Cys Leu Ser Val Phe Tyr Phe Phe Lys Ile Ala Tyr  
       100                  105                  110



Phe Ser His Pro Cys Phe Ile Trp Leu Arg Trp Arg Ile Ser Arg Thr  
 115 120 125  
 Leu Leu Glu Leu Pro Leu Gly Ser Leu Leu Leu Phe Phe Asn Leu  
 130 135 140  
 Ala Leu Thr Gly Gly Leu Ser Asp Leu Trp Ile Asn Ile Tyr Thr Met  
 145 150 155 160  
 Tyr Glu Arg Asn Ser Thr Trp Ser Leu Asp Val Ser Lys Ile Leu Tyr  
 165 170 175  
 Cys Ser Leu Trp Ile Leu Val Ser Leu Ile Tyr Leu Ile Ser Phe Leu  
 180 185 190  
 Leu Ser Leu Ile Ser Leu Leu Leu Leu Ile Leu Ser Leu Met Arg His  
 195 200 205  
 Ile Arg Asn Leu Gln Leu Asn Thr Met Gly Pro Arg Asp Leu Arg Met  
 210 215 220  
 Lys Ala His Lys Arg Ala Met Lys Met Lys Met Lys Met Met Val Ser  
 225 230 235 240  
 Phe Leu Leu Phe Phe Leu Val His Phe Ser Ser Leu Leu Pro Thr Gly  
 245 250 255  
 Trp Ile Phe Leu Ile Gln Gln Lys  
 260

<210> 48  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R27 (hGR27)

<220>  
 <221> MOD\_RES  
 <222> (1)..(264)  
 <223> Xaa = any amino acid

<400> 48  
 Leu Ala Asn Leu Ile Asp Trp Ala Glu Asn Gln Ile Cys Leu Met Asp  
 1 5 10 15  
 Phe Ile Leu Ser Ser Leu Ala Ile Cys Arg Thr Leu Leu Leu Gly Cys  
 20 25 30  
 Cys Val Ala Ile Arg Cys Thr Tyr Asn Asp Tyr Pro Asn Ile Asp Ala  
 35 40 45  
 Val Asn His Asn Leu Ile Lys Ile Ile Thr Ile Phe Asp Ile Leu Arg  
 50 55 60  
 Leu Val Ser Lys Xaa Leu Gly Ile Trp Phe Ala Ser Tyr Leu Ser Ile  
 65 70 75 80

Phe Tyr Leu Leu Lys Val Ala Leu Phe His His Ala Ile Phe Leu Trp  
                     85                    90                    95  
 Leu Lys Trp Arg Ile Ser Arg Ala Val Phe Thr Phe Leu Met Ile Phe  
                     100                    105                    110  
 Leu Phe Phe Tyr Ile Ser Ile Ile Ser Met Ile Lys Ile Lys Leu Phe  
                     115                    120                    125  
 Leu Asp Gln Cys Xaa Tyr Lys Ile Xaa Glu Lys Leu Leu Leu Glu Gly  
                     130                    135                    140  
 Arg Cys Glu Xaa Ser Pro Pro Ser Cys Xaa Pro Asp Ala His Xaa Pro  
                     145                    150                    155                    160  
 Gly Val Val Tyr Ser Leu Tyr His Phe Ser Tyr Leu Met Phe Leu Val  
                     165                    170                    175  
 Cys Tyr Leu Pro Lys Gly Lys His Cys Thr Ala Val Val Ile Gly Asp  
                     180                    185                    190  
 Trp Leu Gln Arg Pro Arg Thr Glu Ala Tyr Val Arg Ala Met Asn Ile  
                     195                    200                    205  
 Met Ile Ala Phe Phe Phe His Leu Leu Tyr Ser Leu Gly Thr Ser Leu  
                     210                    215                    220  
 Ser Ser Val Ser Tyr Phe Leu Cys Lys Arg Lys Ile Val Ala Leu Gly  
                     225                    230                    235                    240  
 Ala Tyr Leu Ser Tyr Pro Leu Ser His Ser Phe Ile Leu Ile Met Glu  
                     245                    250                    255  
 Asn Asn Lys Val Arg Lys Ala Leu  
                     260

<210> 49  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R28 (hGR28)

<400> 49  
 Asn Ile Cys Val Leu Leu Ile Ile Leu Ser Ile Leu Val Val Ser Ala  
     1                    5                    10                    15

Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Ile Asn Val  
                     20                    25                    30

Asn Asp Trp  
                     35

<210> 50  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> human T2R29 (hGR29)

<400> 50

Met Gln Ala Ala Leu Thr Ala Phe Phe Val Leu Leu Phe Ser Leu Leu  
1 5 10 15

Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly  
20 25 30

Lys Glu Trp Leu  
35

<210> 51

<211> 319

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R30 (hGR30)

<400> 51

Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Val Thr  
1 5 10 15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Ser  
20 25 30

Ile Glu Trp Val Lys Thr Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu  
35 40 45

Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu  
50 55 60

His Trp Tyr Ala Asn Val Phe Asn Ser Ala Leu Tyr Ser Ser Glu Val  
65 70 75 80

Gly Ala Val Ala Ser Asn Ile Ser Ala Ile Ile Asn His Phe Ser Ile  
85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn  
100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Arg Ser Val  
115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu  
130 135 140

Ala Val Ile Thr Met Asp Asp Ser Val Trp Thr Lys Glu Tyr Glu Gly  
145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn  
165 170 175

Met Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Ile Leu Thr Leu  
180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile  
 225 230 235 240

Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu  
 245 250 255

Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro  
 260 265 270

Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln  
 275 280 285

Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp Arg  
 290 295 300

Ser Leu Arg Leu His Arg Phe Thr Arg Gly Ala Leu Cys Val Phe  
 305 310 315

<210> 52  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R30 (hGR30)

<400> 52  
 atgataactt ttctacccat catttttttcc attctggtag tggttacatt tgttcttggg 60  
 aatttttcca atggcttcat agctctagta aattccattg agtgggtcaa gacacgaaag 120  
 atctcctcag ctgaccaaatt cctcactgct ctgggtggtct ccagagttgg tttactctgg 180  
 gtcataattat tacattggta tgcaaagtgt ttttaattcag ctttatatag ttcagaagta 240  
 ggagctggtg cttctaatat ctcagcaata atcaaccatt tcagcatctg gcttgctact 300  
 agcctcagca tattttattt gctcaagatt gccaatattt ccaaccttat ttttctccac 360  
 ttaaagaaga gaattaggag tgttggtctg gtgatactgt tgggtccctt ggtatttttg 420  
 atttgtaatc ttgctgtgat aaccatggat gacagtgtgt ggacaaaaga atatgaagga 480  
 aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaaatat gactgtaagc 540  
 aactagcaa acctcatacc cttcattctg accctaatat gttttctgct gttaatctgt 600  
 tctctgtgta aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660  
 accaaggtcc acataaaaagc tttgcaaact gtgacctcct ttcttctggt atgtgccatt 720  
 tactttctgt ccgatgatcat atcagtttgt aattttggga ggctggaaaa gcaacctgtc 780  
 ttcattgttct gccaaactat tatattcagc tatccttcaa cccaccatt catcctgatt 840  
 ttgggaaaca agaagctaaa gcagattttt ctttcagttt tgcggcatgt gaggtactgg 900  
 gtgaaagaca gaagccttcg tctccataga ttcacaagag gggcattgtg tgtctttctg 960

<210> 53  
 <211> 299  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R31 (hGR31)

<220>  
 <221> MOD\_RES  
 <222> (1)..(299)  
 <223> Xaa = any amino acid

<400> 53

Met	Thr	Thr	Phe	Ile	Pro	Ile	Ile	Phe	Ser	Ser	Val	Val	Val	Val	Leu
1				5					10					15	
Phe	Val	Ile	Gly	Asn	Phe	Ala	Asn	Gly	Phe	Ile	Ala	Leu	Val	Asn	Ser
			20					25					30		
Ile	Glu	Arg	Val	Lys	Arg	Gln	Lys	Ile	Ser	Phe	Ala	Asp	Gln	Ile	Leu
		35					40					45			
Thr	Ala	Leu	Ala	Val	Ser	Arg	Val	Gly	Leu	Leu	Trp	Val	Leu	Leu	Leu
	50					55					60				
Asn	Trp	Tyr	Ser	Thr	Val	Phe	Asn	Pro	Ala	Phe	Tyr	Ser	Val	Glu	Val
65					70					75				80	
Arg	Thr	Thr	Ala	Tyr	Asn	Val	Trp	Ala	Val	Thr	Gly	His	Phe	Ser	Asn
			85						90					95	
Trp	Leu	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Ala	Asn
		100						105					110		
Phe	Ser	Asn	Leu	Ile	Phe	Leu	His	Leu	Lys	Arg	Arg	Val	Lys	Ser	Val
		115					120					125			
Ile	Leu	Val	Met	Leu	Leu	Gly	Pro	Leu	Leu	Phe	Leu	Ala	Cys	Gln	Leu
	130					135					140				
Phe	Val	Ile	Asn	Met	Lys	Glu	Ile	Val	Arg	Thr	Lys	Glu	Phe	Glu	Gly
145					150					155				160	
Asn	Met	Thr	Trp	Lys	Ile	Lys	Leu	Lys	Ser	Ala	Met	Tyr	Phe	Ser	Xaa
			165					170						175	
Met	Thr	Val	Thr	Ile	Gly	Ala	Xaa	Leu	Val	Pro	Phe	Thr	Leu	Ser	Leu
		180						185					190		
Ile	Ser	Phe	Leu	Met	Leu	Ile	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys
	195					200						205			
Met	Gln	Leu	His	Gly	Glu	Gly	Ser	Gln	Asp	Leu	Ser	Thr	Lys	Val	His
	210					215					220				
Ile	Lys	Ala	Leu	Gln	Thr	Leu	Ile	Ser	Phe	Leu	Leu	Leu	Cys	Ala	Ile
225				230					235					240	
Phe	Phe	Leu	Phe	Leu	Ile	Val	Ser	Val	Trp	Ser	Pro	Arg	Arg	Leu	Arg
			245						250					255	
Asn	Asp	Pro	Val	Val	Met	Val	Ser	Lys	Ala	Val	Gly	Asn	Ile	Tyr	Leu
		260						265					270		
Ala	Phe	Asp	Ser	Phe	Ile	Leu	Ile	Trp	Arg	Thr	Lys	Lys	Leu	Lys	His
	275					280						285			
Thr	Phe	Leu	Leu	Ile	Leu	Cys	Gln	Ile	Arg	Cys					
	290					295									

<210> 54  
 <211> 900  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R31 (hGR31)

<220>  
 <221> modified\_base  
 <222> (1)..(900)  
 <223> n = g, a, c or t

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<400> 54
atgacaactt ttatacccat cattttttcc agtgtggtag tggttctatt tgttattgga 60
aattttgcta atggcttcat agcattggta aattccattg agcgggtcaa gagacaaaag 120
atctcttttg ctgaccagat tctcactgct ctggcgggtct ccagagttgg ttgctctgg 180
gtattattat taaattggta ttcaactgtg tttaatccag ctttttatag tgtagaagta 240
agaactactg cttataatgt ctgggcagta accggccatt tcagcaactg gcttgctact 300
agcctcagca tattttatgt gctcaagatt gccaatctct ccaaccttat ttttcttcac 360
ttaaagagga gagttaagag tgctattctg gtgatgctgt tggggccttt actatttttg 420
gcttgctaac tttttgtgat aaacatgaaa gagattgtac ggacaaaaga atttgaagga 480
aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcanatat gactgtaacc 540
attggagcan acttagtacc ctttactctg tccctgatat cttttctgat gctaactctgt 600
tctctgtgta aacatctcaa gaagatgcag ctccatggag aaggatcgca agatctcagc 660
accaaggtcc acataaaaagc tttgcaaact ctgatctcct tccctctgtt atgtgccatt 720
ttctttctat tcctaategt ttcggttttg agtcctagga ggctgcggaa tgacccgggt 780
gtcatgggta gcaaggctgt tggaaacata tatcttgcac tcgactcatt catcctaatt 840
tggagaacca agaagctaaa acacaccttt cttttgattt tgtgtcagat taggtgctga 900
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<210> 55  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R32 (hGR32)

```
<400> 55
His Ser Phe Met Leu Thr Met Gly Ser Arg Lys Pro Lys Gln Thr Phe
  1             5             10             15
Leu Ser Ala Leu
                20
```

<210> 56  
 <211> 309  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R33 (hGR33)

```
<400> 56
Met Val Tyr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Phe Ala
  1             5             10             15
Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val
                20             25             30
```

Ile Asp Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Leu  
 35 40 45  
 Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu  
 50 55 60  
 His Trp Tyr Ala Asn Val Phe Asn Ser Ala Leu Tyr Ser Leu Glu Val  
 65 70 75 80  
 Arg Ile Val Ala Ser Asn Ile Ser Ala Val Ile Asn His Phe Ser Ile  
 85 90 95  
 Trp Leu Ala Ala Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn  
 100 105 110  
 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Lys Ser Val  
 115 120 125  
 Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu  
 130 135 140  
 Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly  
 145 150 155 160  
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser  
 165 170 175  
 Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu  
 180 185 190  
 Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Met Leu Cys Ala Ile  
 225 230 235 240  
 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Asn Leu Arg Ser Leu Glu  
 245 250 255  
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro  
 260 265 270  
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln  
 275 280 285  
 Thr Phe Leu Ser Val Phe Trp Gln Val Arg Tyr Trp Val Lys Gly Glu  
 290 295 300  
 Lys Pro Ser Ser Pro  
 305

<210> 57  
 <211> 930  
 <212> DNA  
 <213> Homo sapiens

<220>

<223> human T2R33 (hGR33)

<400> 57

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atggtatatt ttctgcccatt ctttttttcc attctggttag tgtttgcatt tgttcttgga 60
aattttttcca atggcttcat agctctagta aatgtcattg actgggttaa gagacaaaag 120
atctcctcag ctgaccaaatt tctcactgct ctggtggtct ccagagttgg tttactctgg 180
gtcatattat tacattggta tgcaaatgtg tttaattcag ctttatatag tttagaagta 240
agaattggtg cttctaatat ctcagcagta atcaaccatt tcagcatctg gcttgctgct 300
agcctcagca tattttatatt gctcaagatt gccaatcttct ccaaccttat tttctccac 360
ctaaagaaga gaattaagag tgttggtctg gtgatactgt tggggccctt ggtatttctg 420
atgtgtaatc ttgctgtgat aacctggtat gagagagtgt ggacaaaaga atatgaagga 480
aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaagctt gactgtaact 540
actctagcaa acctcatacc ctttactctg agcctaatat gttttctgct gttaactctgt 600
tctctttgta aacatctcaa gaagatgcag ctccatagca aaggatctca agatcccagc 660
accaaggtcc acataaaagc tttgcaaact gtgatctcct tcctcatggt atgtgccatt 720
tactttctgt ccataatgat atcagtttgg aatcttagga gtctggaaaa caaacctgtc 780
ttcatgttct gcaaagctat tagattcagc tatccttcaa tccaccatt catcctgatt 840
tggggaaaca agaagctaaa gcagactttt ctttcagttt tttggcaagt gaggtactgg 900
gtgaaaggag agaagccttc atctccatag 930
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<210> 58

<211> 100

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R34 (hGR34)

<220>

<221> MOD\_RES

<222> (1)..(100)

<223> Xaa = any amino acid

<400> 58

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Gly Ser Ser Arg Xaa Lys Pro Pro Arg Ile Pro His Lys Lys Leu Cys
 1             5             10             15

Lys Leu Gly Pro Ser Phe Pro His Asn Asn Leu Pro Ile Tyr Phe Leu
20             25             30

Cys Xaa Asn His Ile Val Leu Glu Phe Leu Lys Met Arg Pro Lys Lys
35             40             45

Lys Cys Ser Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro Ser
50             55             60

Phe His Ser Phe Ile Leu Xaa Trp Gly Asn Lys Thr Leu Lys Gln Thr
65             70             75             80

Phe Leu Ser Val Xaa Trp Gln Val Thr Cys Trp Ala Lys Gly Gln Asn
85             90             95

Gln Ser Thr Pro
100
```



<210> 59  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R35 (hGR35)

<220>  
 <221> MOD\_RES  
 <222> (1)..(128)  
 <223> Xaa = any amino acid

<400> 59  
 Asn Ala Ile Arg Pro Ser Lys Leu Trp Thr Val Thr Glu Ala Asp Lys  
   1                  5                  10                  15  
 Thr Ser Gln Pro Gly Thr Ser Ala Asn Lys Ile Phe Ser Ala Gly Asn  
           20                  25                  30  
 Leu Ile Ser His Val Asn Met Ser Arg Arg Met Gln Leu His Gly Lys  
       35                  40                  45  
 Gly Ser Gln His Leu Ser Thr Arg Val His Ile Lys Ala Xaa Gln Thr  
   50                  55                  60  
 Val Ile Ser Phe Leu Met Leu Xaa Ala Ile Tyr Phe Leu Cys Leu Ile  
   65                  70                  75                  80  
 Thr Ser Thr Trp Asn Pro Arg Thr Gln Gln Ser Lys Leu Val Phe Leu  
           85                  90                  95  
 Leu Tyr Gln Thr Leu Gly Phe Met Tyr Leu Leu Phe His Ser Phe Ile  
       100                  105                  110  
 Leu Thr Met Gly Ser Arg Lys Pro Lys Gln Thr Phe Leu Ser Ala Leu  
       115                  120                  125

<210> 60  
 <211> 309  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R36 (hGR36)

<400> 60  
 Met Ile Cys Phe Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe Ala  
   1                  5                  10                  15  
 Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val  
       20                  25                  30  
 Ile Asp Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Leu  
       35                  40                  45

Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu  
 50 55 60  
 His Trp Tyr Ser Asn Val Leu Asn Ser Ala Leu Tyr Ser Ser Glu Val  
 65 70 75 80  
 Ile Ile Phe Ile Ser Asn Ala Trp Ala Ile Ile Asn His Phe Ser Ile  
 85 90 95  
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn  
 100 105 110  
 Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val  
 115 120 125  
 Val Leu Val Ile Val Leu Gly Pro Leu Val Phe Leu Val Cys His Leu  
 130 135 140  
 Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Lys Glu Tyr Glu Gly  
 145 150 155 160  
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn  
 165 170 175  
 Leu Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu  
 180 185 190  
 Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile  
 225 230 235 240  
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu  
 245 250 255  
 Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro  
 260 265 270  
 Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln  
 275 280 285  
 Ile Phe Leu Ser Val Phe Trp Gln Met Arg Tyr Trp Val Lys Gly Glu  
 290 295 300  
 Lys Pro Ser Ser Pro  
 305

<210> 61  
 <211> 930  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R36 (hGR36)

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<400> 61
atgatattgtt ttctgctcat cattttatca attctggttag tgtttgcatt tgttcttggga 60
aattttttcca atggcttcat agctctagta aatgtcattg actgggtcaa gagacaaaag 120
atctcctcag ctgaccaaact cctcactgct ctgggtggtct ccagagttgg tttactctgg 180
gtaatattat tacattggta ttcaaagtgt ttgaattcag ctttatatag ttcagaagta 240
ataattttta tttctaattgc ctgggcaata atcaaccatt tcagcatctg gcttgctact 300
agcctcagca tatttttattt gctcaagatc gtcaatttct ccagacttat ttttcatcac 360
ttaaaaagga aggctaagag tgtagttctg gtgatagtgt tgggtccctt ggtatttttg 420
gtttgtcacc ttgtgatgaa acacacgtat ataaatgtgt ggacaaaaga atatgaagga 480
aatgtgactt ggaagatcaa actgaggaat gcaatacacc tttcaaactt gactgtaagc 540
acactagcaa acttgatacc cttcactctg accctgatat cttttctgct gttaatctac 600
tctctgtgta aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660
accaaggtcc acataaaagc tttgcaaact gtgacctcct ttcttctgtt atgtgccatt 720
tactttctgt ccatgatcat atcagtttgt aattttggga ggctggaaaa gcaacctgtc 780
ttcatgttct gccaaagctat tatattcagc tatecttcaa cccaccatt catcctgatt 840
ttgggaaaca agaagctaaa gcagattttt ctttcagttt tttggcaaat gaggtactgg 900
gtgaaaggag agaagccttc atctccatag 930

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<210> 62
<211> 309
<212> PRT
<213> Homo sapiens

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```

<220>
<223> human T2R37 (hGR37)

```

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<220>
<221> MOD_RES
<222> (1)..(309)
<223> Xaa = any amino acid

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<400> 62
Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
  1             5             10             15

Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
      20             25             30

Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ser
      35             40             45

His Cys Ser Gly Gly Val Gln Asn Trp Phe Thr Leu Gly His Ile Ile
      50             55             60

Thr Leu Val Cys Asn Cys Val Xaa Phe Gly Phe Ile Xaa Ile Arg Ser
      65             70             75             80

Lys Asn Phe Trp Phe Xaa Cys Leu Ser Asn Asn Gln Ala Phe Gln His
      85             90             95

Val Gly Val Thr Ser Leu Ser Ile Phe His Leu Leu Lys Thr Ala Asn
      100            105            110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Lys Ser Val
      115            120            125

Gly Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Phe Ile Cys Asn Leu
      130            135            140

```

Phe Val Ile Asn Met Asp Glu Ser Val Trp Thr Lys Glu Tyr Glu Gly  
 145 150 155 160  
 Asn Val Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr His Ser Asn  
 165 170 175  
 Met Thr Leu Thr Met Leu Ala Asn Phe Val Pro Phe Thr Leu Thr Leu  
 180 185 190  
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile  
 225 230 235 240  
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Leu Gly Arg Leu Glu  
 245 250 255  
 Lys Gln Pro Val Phe Met Phe Cys Glu Ala Ile Ile Phe Ser Tyr Pro  
 260 265 270  
 Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln  
 275 280 285  
 Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Gly Glu  
 290 295 300  
 Lys Pro Ser Ser Ser  
 305

<210> 63  
 <211> 930  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T2R37 (hGR37)

<400> 63  
 atgataactt ttctgcccac cattttttcc attctaatag tgggttacatt tgtgattgga 60  
 aatttttgcta atggcttcat agctctagta aattccattg agtggggttaa gagacaaaag 120  
 atctcatcag ctgaccaaatt ttctcactgc tctgggtggtg tccagaattg gtttactctg 180  
 ggtcatatta ttacattggt atgcaactgt gttaatttg gttcatata gattagaagt 240  
 aagaattttt ggttctaattg tctcagcaat aaccaagcat ttcagcatgt ggggtgttact 300  
 agcctcagca tatttcattt gctcaagact gccaatctt ccaaccttat ttttctccac 360  
 ctaaagaaga ggattaagag tgttggtttg gtgatactat tggggccttt gctatttttc 420  
 atttgtaatc tttttgtgat aaacatggat gagagtgtat ggacaaaaga atatgaagga 480  
 aacgtgactt ggaagatcaa attgaggagt gcaatgtacc attcaaatat gactctaacc 540  
 atgctagcaa actttgtacc ctctactctg accctgatat cttttctgct gttaatctgt 600  
 tctctgtgta aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660  
 accaagggtc acataaaagc tttgcaaact gtgacctcct ttcttctggt atgtgccatt 720  
 tactttctgt ccagatcat atcagtttgt aatttgggga ggctggaaaa gcaacctgtc 780  
 ttcattgttct gcgaagctat tatattcagc tatccttcaa cccaccatt catcctgatt 840  
 ttgggaaaca agaagctaaa gcagattttt ctttcagttt tgcggcatgt gaggtactgg 900  
 gtgaaaggag agaagccttc atcttcatag 930

<210> 64  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R38 (hGR38)

<400> 64  
 Met Leu Thr Leu Thr Arg Ile Arg Thr Val Ser Tyr Glu Val Arg Ser  
   1                  5                  10                  15  
 Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr  
                   20                  25                  30  
 Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln  
           35                  40                  45  
 Pro Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg  
       50                  55                  60  
 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His  
   65                  70                  75                  80  
 Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile  
                   85                  90                  95  
 Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys  
           100                  105                  110  
 Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe  
       115                  120                  125  
 Leu Ile Cys Leu Ala Ser Trp Ser Pro Gly Arg Ser Pro Val Pro Ser  
       130                  135                  140

<210> 65  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R39 (hGR39)

<400> 65  
 Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val Arg Asn  
   1                  5                  10                  15  
 Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Leu Pro Leu Ser Val  
       20                  25                  30  
 Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys His Met  
       35                  40                  45  
 His Trp Met Gln Ser Glu Ser His Lys Leu Ser Ser Ala Arg Thr Glu  
       50                  55                  60

Ala His Ile Asn Ala Leu Lys Thr Val Thr Thr Phe Phe Cys Phe Phe  
65 70 75 80  
Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg Ile Pro  
85 90 95  
Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala Ala Tyr  
100 105 110  
Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys Phe Lys  
115 120 125  
Asp Leu Phe Arg Arg Met Ile Cys Leu Gln Lys Glu  
130 135 140

<210> 66  
<211> 71  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human T2R40 (hGR40)

<400> 66  
Ser Gln Tyr Ser Leu Gly His Ser Tyr Val Val Ile Phe Gly Tyr Gly  
1 5 10 15  
Gln Met Lys Lys Thr Phe Leu Gly Ile Leu Trp His Leu Lys Cys Gly  
20 25 30  
Leu Lys Gly Arg Ala Leu Leu Ala Thr Gln Val Gly Leu Arg Glu Lys  
35 40 45  
Ser Thr Arg Ser Leu Gly Val Ile Phe Leu Ala Ser Ser Tyr Ser Phe  
50 55 60  
Phe Val Tyr Val Leu Cys His  
65 70

<210> 67  
<211> 309  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human T2R41 (hGR41)

<220>  
<221> MOD\_RES  
<222> (253)  
<223> Xaa = any amino acid

<400> 67  
Met Ile Thr Phe Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe Ala  
1 5 10 15  
Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val  
20 25 30

Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu  
 35 40 45  
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu  
 50 55 60  
 His Trp Tyr Ala Asn Val Leu Asn Pro Ala Leu Tyr Ser Ser Glu Val  
 65 70 75 80  
 Ile Ile Phe Ile Ser Asn Ile Ser Ala Ile Ile Asn His Phe Ser Ile  
 85 90 95  
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn  
 100 105 110  
 Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val  
 115 120 125  
 Val Leu Val Ile Val Leu Gly Pro Leu Val Phe Leu Val Cys His Leu  
 130 135 140  
 Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Lys Glu Tyr Glu Gly  
 145 150 155 160  
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn  
 165 170 175  
 Leu Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu  
 180 185 190  
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile  
 225 230 235 240  
 Tyr Phe Leu Tyr Leu Ile Thr Ser Thr Trp Asn Leu Xaa Thr Gln Gln  
 245 250 255  
 Ser Lys Leu Val Phe Met Phe Cys Gln Thr Leu Gly Ile Met Tyr Pro  
 260 265 270  
 Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln  
 275 280 285  
 Thr Phe Leu Ser Val Leu Cys Gln Val Thr Cys Leu Val Lys Gly Gln  
 290 295 300  
 Gln Pro Ser Thr Pro  
 305

<210> 68  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R42 (hGR42)

<400> 68  
 Phe Ile Gly Leu Thr Asp Cys Ile Ala Trp Met Arg Asn Gln Lys Leu  
   1                  5                  10                  15  
 Cys Met Val Gly Phe Ile Leu Thr Arg Met Ala Leu Ala Arg Ile Asn  
                   20                  25                  30  
 Ile Leu

<210> 69  
 <211> 297  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R43 (hGR43)

<220>  
 <221> MOD\_RES  
 <222> (1)..(297)  
 <223> Xaa = any amino acid

<400> 69  
 Leu Glu Leu Ile Phe Ser Xaa Lys Val Val Ala Thr Arg Gly Leu Val  
   1                  5                  10                  15  
 Leu Gly Met Leu Gly Asn Gly Leu Ile Gly Leu Val Asn Cys Ile Glu  
                   20                  25                  30  
 Trp Ala Lys Ser Trp Lys Val Ser Ser Ala Asp Phe Ile Leu Thr Ser  
                   35                  40                  45  
 Leu Ala Ile Val Arg Ile Ile Arg Leu Tyr Leu Ile Leu Phe Asp Ser  
                   50                  55                  60  
 Phe Ile Met Val Leu Ser Pro His Leu Tyr Thr Xaa Xaa Xaa Xaa Xaa  
   65                  70                  75                  80  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
                   85                  90                  95  
 Xaa Xaa Ser Leu Ser Ile Phe His Trp Phe Lys Thr Ala Asn Phe Ser  
                   100                  105                  110  
 Asn Leu Ile Phe Leu Pro Leu Lys Glu Glu Asp Xaa Asn Val Trp Leu  
                   115                  120                  125  
 Gly Asp Ala Val Gly Ala Leu Gly Ile Phe His Leu Xaa Ser Cys Ser  
                   130                  135                  140  
 Glu Asn His Gly Xaa Glu Val Cys Gly Gln Lys Asn Met Lys Glu Phe  
   145                  150                  155                  160  
 Cys Ser Gly Met Ile Lys Leu Arg Asn Ala Ile Gln Leu Ser Asn Leu  
                   165                  170                  175



Thr Val Thr Met Pro Ala Asn Val Thr Pro Cys Thr Leu Thr Leu Ile  
 180 185 190  
 Ser Phe Leu Leu Leu Ile Tyr Ser Pro Cys Lys His Val Lys Lys Met  
 195 200 205  
 Gln Leu His Gly Lys Gly Ser Gln His Leu Ser Thr Lys Val His Ile  
 210 215 220  
 Lys Val Leu Gln Thr Val Ile Ser Phe Phe Leu Leu Cys Ala Ile Tyr  
 225 230 235 240  
 Phe Val Ser Val Ile Ile Ser Val Trp Ser Phe Lys Asn Leu Glu Asn  
 245 250 255  
 Lys Pro Val Phe Met Phe Cys Gln Ala Ile Gly Phe Ser Cys Ser Ser  
 260 265 270  
 Ala His Pro Phe Ile Leu Thr Met Gly Asn Lys Lys Leu Lys Gln Thr  
 275 280 285  
 Tyr Leu Ser Val Leu Trp Gln Met Arg  
 290 295

<210> 70  
 <211> 319  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <223> human T2R44 (hGR44)

<400> 70  
 Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Ile  
 1 5 10 15  
 Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser  
 20 25 30  
 Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Val Asp Gln Ile Leu  
 35 40 45  
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu  
 50 55 60  
 His Trp Tyr Ala Thr Gln Leu Asn Pro Ala Phe Tyr Ser Val Glu Val  
 65 70 75 80  
 Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Thr Asn His Phe Ser Ser  
 85 90 95  
 Trp Leu Ala Thr Ser Leu Ser Met Phe Tyr Leu Leu Arg Ile Ala Asn  
 100 105 110  
 Phe Ser Asn Leu Ile Phe Leu Arg Ile Lys Arg Arg Val Lys Ser Val  
 115 120 125  
 Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu  
 130 135 140

Phe Val Ile Asn Met Asp Glu Thr Val Trp Thr Lys Glu Tyr Glu Gly  
 145 150 155 160  
 Asn Val Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr His Ser Asn  
 165 170 175  
 Met Thr Leu Thr Met Leu Ala Asn Phe Val Pro Leu Thr Leu Thr Leu  
 180 185 190  
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile  
 225 230 235 240  
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Leu Gly Arg Leu Glu  
 245 250 255  
 Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro  
 260 265 270  
 Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln  
 275 280 285  
 Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp Arg  
 290 295 300  
 Ser Leu Arg Leu His Arg Phe Thr Arg Gly Ala Leu Cys Val Phe  
 305 310 315

<210> 71  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T2R45 (hGR45)

<400> 71  
 Met Ala Thr Glu Leu Asp Lys Ile Phe Leu Ile Leu Ala Ile Ala Glu  
 1 5 10 15  
 Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys  
 20 25 30  
 Ser Glu Gly Ile Lys Asn Gln Lys Val Phe Ser Ala Asp Phe Ile Leu  
 35 40 45  
 Thr Cys Leu Ala Ile Ser Thr Ile Gly Gln Leu Leu Val Ile Leu Phe  
 50 55 60  
 Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg  
 65 70 75 80  
 Leu Gly Lys Thr Val Ile Met Leu Trp His Met Thr Asn His Leu Thr  
 85 90 95

Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala  
 100 105 110  
 His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly  
 115 120 125  
 Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp  
 130 135 140  
 Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp  
 145 150 155 160  
 Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp  
 165 170 175  
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro  
 180 185 190  
 Phe Ser Leu Phe Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val  
 195 200 205  
 Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser  
 210 215 220  
 Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu  
 225 230 235 240  
 Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Trp Ile  
 245 250 255  
 Phe Phe Met Leu Trp Asn Asn Lys Cys Ile Lys Phe Val Met Leu Ala  
 260 265 270  
 Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn  
 275 280 285  
 Ser Lys Leu Gln Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn  
 290 295 300  
 Tyr Thr Lys Thr Pro Asn Pro Leu Pro Leu  
 305 310

<210> 72

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R46 (hGR46)

<400> 72

Met Ser Phe Leu His Ile Val Phe Ser Ile Leu Val Val Val Ala Phe  
 1 5 10 15  
 Ile Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Ile Asn Phe Ile  
 20 25 30  
 Ala Trp Val Lys Lys Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile Ala  
 35 40 45

Asp Lys Gln Ser Pro Glu Leu Val Cys Ser Gly  
50 55

<210> 73  
<211> 65  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human T2R47 (hGR47)

<220>  
<221> MOD\_RES  
<222> (1)..(65)  
<223> Xaa = any amino acid

<400> 73  
Met Leu Asn Ala Leu Tyr Ser Ile Leu Ile Ile Ile Ile Asn Ile Xaa  
1 5 10 15

Phe Leu Ile Gly Ile Leu Gly Asn Gly Phe Ile Thr Leu Val Asn Gly  
20 25 30

Ile Asp Trp Val Lys Met Xaa Lys Arg Ser Ser Ile Leu Thr Ala Leu  
35 40 45

Thr Ile Ser Arg Ile Cys Leu Ile Ser Val Ile Met Val Arg Trp Phe  
50 55 60

Ile  
65

<210> 74  
<211> 60  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human T2R48 (hGR48)

<400> 74  
Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu His Trp Tyr Ser  
1 5 10 15

Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val Ile Ile Phe Ile  
20 25 30

Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile Trp Leu Ala Thr  
35 40 45

Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn  
50 55 60

<210> 75  
<211> 72  
<212> PRT  
<213> Homo sapiens

<220>

<223> human T2R49 (hGR49)

<400> 75

Thr Val Thr Met Leu Ala Asn Leu Val Pro Phe Thr Val Thr Leu Ile  
1 5 10 15  
Ser Phe Leu Leu Leu Val Cys Ser Leu Cys Lys His Leu Lys Lys Met  
20 25 30  
His Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile  
35 40 45  
Lys Val Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile Tyr  
50 55 60  
Phe Val Ser Val Ile Ile Ser Ser  
65 70

<210> 76

<211> 299

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R50 (hGR50)

<400> 76

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20 25 30  
Thr Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Val  
35 40 45  
Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu  
50 55 60  
Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu  
65 70 75 80  
Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Thr Gly His Phe Ser Asn  
85 90 95  
Trp Pro Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn  
100 105 110  
Phe Ser Asn Leu Ile Phe Leu Arg Leu Lys Arg Arg Val Lys Ser Val  
115 120 125  
Ile Leu Val Val Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu  
130 135 140  
Phe Val Val Asn Met Asn Gln Ile Val Trp Thr Lys Glu Tyr Glu Gly  
145 150 155 160  
Asn Met Thr Trp Lys Ile Lys Leu Arg Arg Ala Met Tyr Leu Ser Asp  
165 170 175

Thr Thr Val Thr Met Leu Ala Asn Leu Val Pro Phe Thr Val Thr Leu  
 180 185 190  
 Ile Ser Phe Leu Leu Leu Val Cys Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Val Leu Gln Thr Val Ile Ser Phe Phe Leu Leu Cys Ala Ile  
 225 230 235 240  
 Tyr Phe Val Ser Val Ile Ile Ser Val Trp Ser Phe Lys Asn Leu Glu  
 245 250 255  
 Asn Lys Pro Val Phe Met Phe Cys Gln Ala Ile Gly Phe Ser Cys Ser  
 260 265 270  
 Ser Ala His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln  
 275 280 285  
 Thr Tyr Leu Ser Val Leu Trp Gln Met Arg Tyr  
 290 295

<210> 77  
 <211> 335  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R01 (rGR01)

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 Ile Asp Leu Ile Met Trp Lys Lys Met Ala Pro Leu Asp Leu Leu Leu  
 35 40 45  
 Phe Cys Leu Ala Thr Ser Arg Ile Ile Leu Gln Leu Cys Ile Leu Phe  
 50 55 60  
 Ala Gln Leu Cys Leu Phe Ser Leu Val Arg His Thr Leu Phe Glu Asp  
 65 70 75 80  
 Asn Ile Thr Phe Val Phe Ile Ile Asn Glu Leu Ser Leu Trp Phe Ala  
 85 90 95  
 Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Ile Ala Thr Ile Pro His  
 100 105 110  
 Pro Leu Phe Leu Trp Leu Lys Met Arg Ile Ser Arg Leu Val Pro Trp  
 115 120 125  
 Leu Ile Leu Gly Ser Val Leu Tyr Val Ile Ile Thr Thr Phe Ile His  
 130 135 140

Ser Arg Glu Thr Ser Ala Ile Leu Lys Pro Ile Phe Ile Ser Leu Phe  
 145 150 155 160  
 Pro Lys Asn Ala Thr Gln Val Gly Thr Gly His Ala Thr Leu Leu Ser  
 165 170 175  
 Val Leu Val Leu Gly Leu Thr Leu Pro Leu Phe Ile Phe Thr Val Ala  
 180 185 190  
 Val Leu Leu Leu Ile Tyr Ser Leu Trp Asn Tyr Ser Arg Gln Met Arg  
 195 200 205  
 Thr Met Val Gly Thr Arg Glu Tyr Ser Gly His Ala His Ile Ser Ala  
 210 215 220  
 Met Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Leu Ser His Tyr Met  
 225 230 235 240  
 Val Ala Val Leu Ile Ser Thr Gln Val Leu Tyr Leu Gly Ser Arg Thr  
 245 250 255  
 Phe Val Phe Cys Leu Leu Val Ile Gly Met Tyr Pro Ser Ile His Ser  
 260 265 270  
 Ile Val Leu Ile Leu Gly Asn Pro Lys Leu Lys Arg Asn Ala Lys Met  
 275 280 285  
 Phe Ile Val His Cys Lys Cys Cys His Cys Thr Arg Ala Trp Val Thr  
 290 295 300  
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 305 310 315 320  
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 325 330 335

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 <211> 1331  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T2R01 (rGR01)

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 gcagtttgtc actggggtct tggcaaatgg cctcattgtg gttgtccatg ctattgactt 180  
 gatcatgtgg aagaaaaatgg ccccgttgga tctgcttcta ttttgccctg cgacttctcg 240  
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 aacctttgta ttctgcttac tggttattgg tatgtacccc tcaatacact cgattgtctt 900

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<210> 79

<211> 333

<212> PRT

<213> Rattus sp.

<220>

<223> rat T2R02 (rGR02)

<400> 79

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              20              25              30

Ala Leu Val Asn Ile Met Asp Trp Leu Lys Arg Arg Arg Ile Ser Thr
              35              40              45

Ala Asp Gln Ile Leu Thr Ala Leu Ala Leu Thr Arg Leu Ile Tyr Val
              50              55              60

Trp Ser Val Leu Ile Cys Ile Leu Leu Leu Phe Leu Cys Pro His Leu
  65              70              75              80

Ser Met Arg Pro Glu Met Phe Thr Ala Ile Gly Val Ile Trp Val Val
              85              90              95

Asp Asn His Phe Ser Ile Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
              100              105              110

Phe Leu Lys Ile Ala Ser Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
              115              120              125

Trp Arg Val Lys Lys Val Val Leu Met Ile Ile Leu Ile Ser Leu Ile
              130              135              140

Phe Leu Met Leu Asn Ile Ser Ser Leu Gly Met Tyr Asp His Phe Ser
  145              150              155              160

Ile Asp Val Tyr Glu Gly Asn Met Ser Tyr Asn Leu Val Asp Ser Thr
              165              170              175

His Phe Pro Arg Ile Phe Leu Phe Thr Asn Ser Ser Lys Val Phe Leu
              180              185              190

Ile Ala Asn Ser Ser His Val Phe Leu Pro Ile Asn Ser Leu Phe Met
              195              200              205

Leu Ile Pro Phe Thr Val Ser Leu Val Ala Phe Phe Val Leu Phe Leu
  210              215              220

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Ser Leu Trp Lys His His Lys Lys Met Gln Val Asn Ala Lys Gly Pro  
 225 230 235 240  
 Arg Asp Ala Ser Thr Met Ala His Thr Lys Ala Leu Gln Ile Gly Phe  
 245 250 255  
 Ser Phe Leu Leu Leu Tyr Ala Ile Tyr Leu Leu Phe Ile Ile Thr Gly  
 260 265 270  
 Ile Leu Asn Leu Asp Leu Met Arg Cys Ile Val Ile Leu Leu Phe Asp  
 275 280 285  
 His Ile Ser Gly Ala Val Phe Ser Ile Ser His Ser Phe Val Leu Ile  
 290 295 300  
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 305 310 315 320  
 Leu Arg Cys Arg Ser Lys Asp Met Asp Thr Val Val Phe  
 325 330

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 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T2R02 (rGR02)

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<210> 81  
 <211> 299  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R03 (rGR03)

<400> 81

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Glu	Ser	Leu	Val	Ile	Ile	Val	Gln	Ser	Cys	Thr	Thr	Val	Ala	Val	Leu	20	25	30	
Phe	Arg	Glu	Trp	Met	His	Phe	Gln	Arg	Leu	Ser	Pro	Val	Glu	Ile	Ile	35	40	45	
Leu	Ile	Ser	Leu	Gly	Ile	Ser	His	Phe	Cys	Leu	Gln	Trp	Thr	Ser	Met	50	55	60	
Leu	Tyr	Asn	Phe	Gly	Thr	Tyr	Ser	Arg	Pro	Val	Leu	Leu	Phe	Trp	Lys	65	70	75	80
Val	Ser	Val	Val	Trp	Glu	Phe	Met	Asn	Val	Leu	Thr	Phe	Trp	Leu	Thr	85	90	95	
Ser	Leu	Leu	Ala	Val	Leu	Tyr	Cys	Val	Lys	Val	Ser	Ser	Phe	Ser	His	100	105	110	
Pro	Val	Phe	Leu	Trp	Leu	Arg	Leu	Lys	Ile	Leu	Lys	Leu	Val	Leu	Trp	115	120	125	
Leu	Leu	Leu	Gly	Ala	Leu	Ile	Ala	Ser	Cys	Leu	Ser	Ile	Ile	Pro	Ser	130	135	140	
Val	Val	Lys	Tyr	His	Ile	Gln	Met	Glu	Leu	Leu	Thr	Leu	Asp	His	Leu	145	150	155	160
Pro	Lys	Asn	Ser	Ser	Leu	Ile	Leu	Arg	Leu	Gln	Met	Phe	Glu	Trp	Tyr	165	170	175	
Phe	Ser	Asn	Pro	Phe	Lys	Met	Ile	Gly	Phe	Gly	Val	Pro	Phe	Leu	Val	180	185	190	
Phe	Leu	Ile	Ser	Ile	Ile	Leu	Leu	Thr	Val	Ser	Leu	Val	Gln	His	Trp	195	200	205	

Gly Gln Met Lys His Tyr Ser Ser Ser Ser Ser Ser Leu Arg Ala Gln  
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 Cys Thr Val Leu Lys Ser Leu Ala Thr Phe Phe Ile Phe Phe Thr Ser  
 225 230 235 240  
 Tyr Phe Leu Thr Ile Val Val Ser Phe Ile Gly Thr Val Phe Asp Lys  
 245 250 255  
 Lys Ser Trp Phe Trp Val Cys Glu Ala Val Ile Tyr Gly Leu Val Cys  
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 275 280 285  
 Leu Arg Leu Gln Phe Trp Ser Pro Glu Ser Ser  
 290 295

<210> 82  
 <211> 6552  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T2R03 (rGR03)

<220>  
 <221> modified\_base  
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 <223> n = g, a, c or t

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 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R04 (rGR04)

<400> 83

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Met Glu Tyr Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Ile Leu
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Ile Gly Leu Ala Ile Ser Arg Ile Gly Val Val Trp Ile Ile Ile Leu
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Gln Gly Tyr Met Gln Val Phe Phe Pro His Ile Leu Thr Phe Gly Asn
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Ile Thr Glu Tyr Ile Thr Tyr Ile Trp Val Phe Leu Asn His Leu Ser
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Val Trp Phe Ala Thr Asn Leu Asn Ile Leu Tyr Phe Leu Lys Ile Ala
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Asn Phe Ser Asn Ser Val Phe Leu Trp Leu Lys Ser Arg Val Arg Val
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Val Phe Ile Phe Leu Ser Gly Cys Leu Leu Thr Ser Trp Leu Leu Cys
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Phe Pro Gln Phe Ser Lys Met Leu Asn Asn Ser Lys Met Tyr Trp Gly
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 Thr Cys Phe Leu Leu Ile Val Phe Leu Trp Arg His Ile Arg Gln Met  
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 His Ser Asp Gly Ser Gly Leu Arg Asp Leu Asn Thr Glu Ala His Val  
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 Lys Ala Met Arg Val Leu Ile Ser Phe Ala Val Leu Phe Ile Leu His  
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<212> PRT

<213> Rattus sp.

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<223> rat T2R05 (rGR05)

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Thr Gly Leu Ala Ile Ser Arg Ile Cys Leu Val Trp Ile Leu Ile Thr  
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Glu Ala Tyr Ile Lys Ile Phe Ser Pro Gln Leu Leu Ser Pro Ile Asn  
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 <213> Rattus sp.

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 <223> rat T2R06 (rGR06)

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           35                    40                    45  
 Leu Asp Cys Ile Ile Leu Val Gln Tyr Pro Asp Thr Tyr Asn Arg Gly  
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 Lys Glu Met Arg Ile Ile Asp Phe Phe Trp Thr Leu Thr Asn His Leu  
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 225 230 235 240  
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 245 250 255  
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<220>  
 <223> rat T2R06 (rGR06)

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 <212> PRT  
 <213> Rattus sp.

<220>  
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 Ile Ala Trp Leu Ser Lys Arg Thr Leu Ser Phe Ile Gly Trp Ile Gln  
                   35                  40                  45  
 Leu Phe Leu Ala Ile Ser Arg Val Val Leu Ile Trp Glu Met Leu Leu  
           50                  55                  60  
 Ala Trp Leu Lys Tyr Met Lys Tyr Ser Phe Ser Tyr Leu Ala Gly Thr  
           65                  70                  75                  80  
 Glu Leu Arg Val Met Met Leu Thr Trp Val Val Ser Asn His Phe Ser  
                   85                  90                  95  
 Leu Trp Leu Ala Thr Ile Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala  
                   100                  105                  110  
 Ser Phe Ser Arg Pro Val Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys  
           115                  120                  125  
 Val Leu Leu Leu Ile Leu Leu Gly Asn Leu Ile Phe Leu Met Phe Asn  
           130                  135                  140  
 Ile Leu Gln Ile Asn Thr His Ile Glu Asp Trp Met Asp Gln Tyr Lys  
           145                  150                  155                  160  
 Arg Asn Ile Thr Trp Asp Ser Arg Val Asn Glu Phe Val Gly Phe Ser  
                   165                  170                  175  
 Asn Leu Val Leu Leu Glu Met Ile Met Phe Ser Val Thr Pro Phe Thr  
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 Val Ala Leu Val Ser Phe Ile Leu Leu Ile Phe Ser Leu Trp Lys His  
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 Leu Gln Lys Met His Leu Ser Ser Arg Gly Glu Arg Asp Pro Ser Thr  
           210                  215                  220  
 Lys Ala His Val Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu  
           225                  230                  235                  240  
 Tyr Ala Thr Tyr Phe Ile Ser Phe Phe Ile Ser Leu Ile Pro Met Ala  
                   245                  250                  255  
 His Lys Lys Gly Leu Asp Leu Met Phe Ser Leu Thr Val Gly Leu Phe  
                   260                  265                  270

Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly His Ser Asn Leu  
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Arg His Ser Ser Cys Leu Val Ile Thr Tyr Leu Arg Cys Lys Glu Lys  
 290 295 300

Asp  
 305

<210> 90  
 <211> 3994  
 <212> DNA  
 <213> Rattus sp.

<220>  
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<220>  
 <221> modified\_base  
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 <213> Rattus sp.

<220>  
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           20                    25                    30  
 Trp Asp Trp Val Val Lys Arg Lys Leu Ser Thr Ile Asp Lys Ile Leu  
           35                    40                    45  
 Leu Thr Leu Ala Ile Ser Arg Ile Thr Leu Ile Trp Glu Met Tyr Ala  
       50                    55                    60  
 Cys Phe Lys Ile Val Tyr Gly Ser Ser Ser Phe Ile Phe Gly Met Lys  
       65                    70                    75                    80  
 Leu Gln Ile Leu Tyr Phe Ala Trp Ile Leu Ser Ser His Phe Ser Leu  
           85                    90                    95  
 Trp Phe Ala Thr Ala Leu Ser Ile Phe Tyr Leu Leu Arg Ile Ala Asn  
      100                    105                    110

Cys Ser Trp Lys Ile Phe Leu Tyr Leu Lys Trp Arg Leu Lys Gln Val  
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 Ile Val Gly Met Leu Leu Ala Ser Leu Val Phe Leu Pro Gly Ile Leu  
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 Met Gln Arg Thr Leu Glu Glu Arg Pro Tyr Gln Tyr Gly Gly Asn Thr  
 145 150 155 160  
 Ser Glu Asp Ser Met Glu Thr Asp Phe Ala Lys Phe Thr Glu Leu Ile  
 165 170 175  
 Leu Phe Asn Met Thr Ile Phe Ser Val Ile Pro Phe Ser Leu Ala Leu  
 180 185 190  
 Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln Lys  
 195 200 205  
 Met Gln Leu Ser Ser Arg Gly His Gly Asp Pro Ser Thr Lys Ala His  
 210 215 220  
 Arg Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu Tyr Thr Ser  
 225 230 235 240  
 Tyr Phe Leu Ser Leu Leu Ile Ser Trp Ile Ala Gln Lys His His Ser  
 245 250 255  
 Lys Leu Val Asp Ile Ile Gly Ile Ile Thr Glu Leu Met Tyr Pro Ser  
 260 265 270  
 Val His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr  
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<210> 92  
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 <212> DNA  
 <213> Rattus sp.

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 <223> n = g, a, c or t

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 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R09 (rGR09)

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 35 40 45  
 Phe Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Ile Leu Ile Leu  
 50 55 60  
 Asp Ala Tyr Ala Lys Leu Phe Phe Pro Gly Lys Tyr Leu Ser Lys Ser  
 65 70 75 80  
 Leu Thr Glu Ile Ile Ser Cys Ile Trp Met Thr Val Asn His Met Thr  
 85 90 95  
 Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala  
 100 105 110  
 Asn Phe Ser His Tyr Ile Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys  
 115 120 125

Val Phe Ala Phe Leu Leu Trp Cys Leu Leu Ile Ser Trp Ala Ile Ser  
 130 135 140  
 Phe Ser Phe Thr Val Lys Val Met Lys Ser Asn Pro Lys Asn His Gly  
 145 150 155 160  
 Asn Arg Thr Ser Gly Thr His Trp Glu Lys Arg Glu Phe Thr Ser Asn  
 165 170 175  
 Tyr Val Leu Ile Asn Ile Gly Val Ile Ser Leu Leu Ile Met Thr Leu  
 180 185 190  
 Thr Ala Cys Phe Leu Leu Ile Ile Ser Leu Trp Lys His Ser Arg Gln  
 195 200 205  
 Met Gln Ser Asn Val Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His  
 210 215 220  
 Val Lys Ala Ile Lys Phe Leu Ile Ser Phe Ile Ile Leu Phe Ile Leu  
 225 230 235 240  
 Tyr Phe Ile Gly Val Ala Val Glu Ile Ile Cys Met Phe Ile Pro Glu  
 245 250 255  
 Asn Lys Leu Leu Phe Ile Phe Gly Leu Thr Thr Ala Ser Val Tyr Pro  
 260 265 270  
 Cys Cys His Ser Val Ile Leu Ile Leu Thr Asn Ser Gln Leu Lys Gln  
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 <211> 2596  
 <212> DNA  
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aagttctttt ttttacatct ttattaaatt ggggtatttct tatttacatt tcaaagtga 2520
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ccctcgtgcc gaattc 2596

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<210> 95  
 <211> 137  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R10 (rGR10)

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<400> 95
Met Phe Leu His Thr Ile Lys Gln Arg Asp Ile Phe Thr Leu Ile Ile
  1               5               10               15

Ile Phe Phe Val Glu Ile Thr Met Gly Ile Leu Gly Asn Gly Phe Ile
      20               25               30

Ala Leu Val Asn Ile Val Asp Trp Ile Lys Arg Arg Arg Ile Ser Ser
      35               40               45

Val Asp Lys Ile Leu Thr Thr Leu Ala Leu Thr Arg Leu Ile Tyr Ala
      50               55               60

Trp Ser Met Leu Ile Phe Ile Leu Leu Phe Ile Leu Gly Pro His Leu
      65               70               75               80

Ile Met Arg Ser Glu Ile Leu Thr Ser Met Gly Val Ile Trp Val Val
      85               90               95

Asn Asn His Phe Ser Ile Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
      100               105               110

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Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys  
 115 120 125

Trp Arg Val Lys Lys Val Val Leu Met  
 130 135

<210> 96  
 <211> 818  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T2R10 (rGR10)

<400> 96  
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 gggaatcaaa tttccttcct gataggcttag cttatgagaa ttcagcatct tattcaactt 180  
 cagaaaattg gatataagat acagtgtctg gatgaagccg aattgatcta tttggggaga 240  
 aaaaacgccca acattttataa taagggtttta tgagacagtt cctgggaaat ttggatattt 300  
 cctagttagt aatgtgtataa tgggattttta aaacatgatt attttgtatt tttaacaacc 360  
 aacatgagga gcttttttaa tgccacttag acattataaa ctgaagcatg ttcttacaca 420  
 caataaagca acgtgatatt tttactttga taatcatatt ttttgtggaa ataacaatgg 480  
 gaatcttagg aaatggattc atagcactag tgaacattgt ggactggatc aagagaagaa 540  
 ggattttcttc agtggataag attctcacta ccttggccct taccagactc atttatgcgt 600  
 ggtctatgct cattttttata ttgttattca tactgggccc gcatttgatt atgagatcag 660  
 aaatacttac atcaatgggt gttatctggg tggatgaacaa tcacttcagc atctggcttg 720  
 ctacatgcct cgggtgtcttt tattttctca agatagccaa tttttctaac tctttgtttc 780  
 tttacctaataa gtggagaggt aaaaaagtgg ttttaagt 818

<210> 97  
 <211> 105  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R11 (rGR11)

<220>  
 <221> MOD\_RES  
 <222> (101)  
 <223> Xaa = any amino acid

<400> 97  
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 1 5 10 15  
 Lys Ser Lys Lys Ile Ser Leu Ser Asp Phe Ile Ile Thr Ser Leu Ala  
 20 25 30  
 Leu Phe Arg Ile Phe Leu Leu Trp Ile Ile Phe Thr Asp Ser Leu Ile  
 35 40 45  
 Ile Val Phe Ser Tyr His Ala His Asp Ser Gly Ile Arg Met Gln Leu  
 50 55 60  
 Ile Asp Val Phe Trp Thr Phe Thr Thr His Phe Ser Ile Trp Leu Ile  
 65 70 75 80

Ser Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile Ala Thr Phe Ser His  
85 90 95

Pro Ser Phe Leu Xaa Leu Lys Ser Arg  
100 105

<210> 98  
<211> 315  
<212> DNA  
<213> Rattus sp.

<220>  
<223> rat T2R11 (rGR11)

<400> 98  
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atttctttgt ctgacttcat cattaccage ttggccctct tcaggatctt tctgctgtgg 120  
atcatcttta ctgatagcct cataatagtg ttctottacc acgcccacga ctcagggata 180  
aggatgcaac ttattgatgt tttctggaca tttacaaccc acttcagtat ttggcttatt 240  
tcctgtctca gtgtttcta ctgcctgaaa atagccactt tctcccaccc ctcattcctg 300  
tagctcaaat ctaga 315

<210> 99  
<211> 308  
<212> PRT  
<213> Rattus sp.

<220>  
<223> rat T2R12 (rGR12)

<400> 99  
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1 5 10 15  
Cys Phe Leu Gly Ile Leu Ala Asn Gly Phe Ile Val Leu Met Leu Ser  
20 25 30  
Arg Glu Trp Leu Trp Arg Gly Arg Leu Leu Pro Ser Asp Met Ile Leu  
35 40 45  
Leu Ser Leu Gly Thr Ser Arg Phe Cys Gln Gln Cys Val Gly Leu Val  
50 55 60  
Asn Ser Phe Tyr Tyr Ser Leu His Leu Val Glu Tyr Ser Arg Ser Leu  
65 70 75 80  
Ala Arg Gln Leu Ile Ser Leu His Met Asp Phe Leu Asn Ser Ala Thr  
85 90 95  
Phe Trp Phe Gly Thr Trp Leu Ser Val Leu Phe Cys Ile Lys Ile Ala  
100 105 110  
Asn Phe Ser His Pro Ala Phe Leu Trp Leu Lys Trp Arg Phe Pro Ala  
115 120 125  
Leu Val Pro Trp Leu Leu Leu Gly Ser Ile Leu Val Ser Phe Ile Val  
130 135 140

Thr Leu Met Phe Phe Trp Gly Asn His Thr Val Tyr Gln Ala Phe Leu  
145 150 155 160

Arg Arg Lys Phe Ser Gly Asn Thr Thr Phe Lys Glu Trp Asn Arg Arg  
165 170 175

Leu Glu Ile Asp Tyr Phe Met Pro Leu Lys Leu Val Thr Thr Ser Ile  
180 185 190

Pro Cys Ser Leu Phe Leu Val Ser Ile Leu Leu Leu Ile Asn Ser Leu  
195 200 205

Arg Arg His Ser Gln Arg Met Gln His Asn Ala His Ser Leu Gln Asp  
210 215 220

Pro Asn Thr Gln Ala His Ser Arg Ala Leu Lys Ser Leu Ile Ser Phe  
225 230 235 240

Leu Val Leu Tyr Ala Leu Ser Tyr Val Ser Met Val Ile Asp Ala Thr  
245 250 255

Val Val Ile Ser Ser Asp Asn Val Trp Tyr Trp Pro Trp Gln Ile Ile  
260 265 270

Leu Tyr Leu Cys Met Ser Val His Pro Phe Ile Leu Ile Thr Asn Asn  
275 280 285

Leu Lys Phe Arg Gly Thr Phe Arg Gln Leu Leu Leu Leu Ala Arg Gly  
290 295 300

Phe Trp Val Thr  
305

<210> 100  
<211> 1295  
<212> DNA  
<213> Rattus sp.

<220>  
<223> rat T2R12 (rGR12)

<400> 100  
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tctgtttcct gggaatcctg gcaaacggct tcattgtgct gatgctgagc agggaatggc 180  
tatggcgcggt taggctgctc ccctcagaca tgatcctcct cagtttgggc acctcccgat 240  
tctgccagca gtgcgttggg ctggtgaaca gtttctacta ttccctccac cttgttgagt 300  
actccaggag ccttgcccgt caactcatta gtcttcacat ggacttcttg aactcagcca 360  
ctttctgggt tggcacctgg ctcagcgtcc tgttctgtat caagattgct aacttctccc 420  
atcctgcctt cctgtgggtg aagtggagat tcccagcatt ggtgccttgg ctccactagg 480  
gctctatctt ggtgtccttc atcgtaactc tgatgttctt ttggggaaac cacactgtct 540  
atcaggcatt cttaaggaga aagttttctg ggaacacaaac ctttaaggag tggaacagaa 600  
ggctggaaat agactatttc atgcctctga aacttgtcac cacgtcaatt ccttgctctc 660  
tttttctagt ctcaattttg ctgttgatca atttctcag aaggcattca caaagaatgc 720  
agcacaatgc tcacagcttg caagacccca acaccaggc tcacagcaga gcctgaagt 780  
cactcatctc atttctgggt ctttacgcgc tgtcctatgt gtccatgggtc attgacgcta 840  
cagttgtcat ctctcagat aacgtgtggt attggccctg gcaaattata ctttacttgt 900  
gcattgtccgt acatccattt atccttatca ctaataatct caagttccga ggcaccttca 960  
ggcagctact cctgttggcc aggggattct ggggtgacct gaaggtttgg tctctttatc 1020  
tgtacccttt gaagagactt aggtgagggt gacttccctt ggaagtgatc tcactacat 1080

ggaaatgtct ttgtaggctg acatgggggc atactatgtg gttcctcctt gggaaagagg 1140  
 agaagaaaaat acagggattc tgagcgttct tccttatctt gggatattat gaaaatggac 1200  
 attctgaatc ctgaaccagt attgatctga agtgcaaagt acaatatgcc tgttccttc 1260  
 atgtctgcta tcctcttggt acttattaat tccct 1295

<210> 101  
 <211> 332  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T2R13 (rGR13)

<400> 101  
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 20 25 30  
 Asn Val Phe Ile Gly Leu Val Asn Tyr Ser Asp Trp Val Lys Asn Lys  
 35 40 45  
 Lys Ile Thr Phe Ile Asn Phe Ile Leu Ile Cys Leu Ala Ala Ser Arg  
 50 55 60  
 Ile Ser Ser Val Leu Val Val Phe Ile Asp Ala Ile Ile Leu Glu Leu  
 65 70 75 80  
 Thr Pro His Val Tyr His Ser Tyr Ser Arg Val Lys Cys Ser Asp Ile  
 85 90 95  
 Phe Trp Val Ile Thr Asp Gln Leu Ser Thr Trp Leu Ala Thr Cys Leu  
 100 105 110  
 Ser Ile Phe Tyr Leu Leu Lys Ile Ala His Phe Ser His Pro Leu Phe  
 115 120 125  
 Leu Trp Leu Lys Trp Arg Leu Arg Gly Val Leu Val Gly Phe Leu Leu  
 130 135 140  
 Phe Ser Leu Phe Ser Leu Ile Val Tyr Phe Leu Leu Leu Glu Leu Leu  
 145 150 155 160  
 Ser Ile Trp Gly Asp Ile Tyr Val Ile Pro Lys Ser Asn Leu Thr Leu  
 165 170 175  
 Tyr Ser Glu Thr Ile Lys Thr Leu Ala Phe Gln Lys Ile Ile Val Phe  
 180 185 190  
 Asp Met Leu Tyr Leu Val Pro Phe Leu Val Ser Leu Ala Ser Leu Leu  
 195 200 205  
 Leu Leu Phe Leu Ser Leu Val Lys His Ser Gln Asn Leu Asp Arg Ile  
 210 215 220  
 Ser Thr Thr Ser Glu Asp Ser Arg Ala Lys Ile His Lys Lys Ala Met  
 225 230 235 240



<400> 103  
Val Ala Asn Ile Met Asp Trp Val Lys Arg Arg Lys Leu Ser Ala Val  
1 5 10 15  
Asp Gln Leu Leu Thr Val Leu Ala Ile Ser Arg Ile Thr Leu Leu Trp  
20 25 30  
Ser Leu Tyr Ile Leu Lys Ser Thr Phe Ser Met Val Pro Asn Phe Glu  
35 40 45  
Val Ala Ile Pro Ser Thr Arg Leu Thr Asn Leu Val Trp Ile Ile Ser  
50 55 60  
Asn His Phe Asn  
65

<210> 104  
<211> 206  
<212> DNA  
<213> Rattus sp.

<220>  
<223> rat T2R14 (rGR14)

<400> 104  
ctgtggcaaa cataatggat tgggtcaaga gaaggaagct ctctgcagtg gatcagctcc 60  
tcactgtgct ggccatctcc agaatcactc tgttgtgggc attgtacata ctgaaatcaa 120  
cattttcaat ggtgccaaac tttgaggtag ctataccgtc aacaagacta actaatcttg 180  
tctggataat ttctaaccat tttaat 206

<210> 105  
<211> 327  
<212> PRT  
<213> Mus sp.

<220>  
<223> mouse T2R01 (mGR01)

<400> 105  
Met Gln His Leu Leu Lys Thr Ile Phe Val Ile Cys His Ser Thr Leu  
1 5 10 15  
Ala Ile Ile Leu Ile Phe Glu Leu Ile Ile Gly Ile Leu Gly Asn Gly  
20 25 30  
Phe Met Ala Leu Val His Cys Met Asp Trp Val Lys Arg Lys Lys Met  
35 40 45  
Ser Leu Val Asn Lys Ile Leu Thr Ala Leu Ala Ile Ser Arg Ile Phe  
50 55 60  
His Leu Ser Leu Leu Leu Ile Ser Leu Val Ile Phe Phe Ser Tyr Ser  
65 70 75 80  
Asp Ile Pro Met Thr Ser Arg Met Thr Gln Val Ser Asn Asn Val Trp  
85 90 95  
Ile Ile Val Asn His Phe Ser Ile Trp Leu Ser Thr Cys Leu Ser Val  
100 105 110

Leu Tyr Phe Leu Lys Ile Ser Asn Phe Ser Asn Ser Phe Phe Leu Tyr  
 115 120 125  
 Leu Lys Trp Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser  
 130 135 140  
 Leu Leu Leu Leu Ile Leu Asn Ile Leu Leu Ile Asn Leu Glu Ile Ser  
 145 150 155 160  
 Ile Cys Ile Lys Glu Cys Gln Arg Asn Ile Ser Cys Ser Phe Ser Ser  
 165 170 175  
 His Tyr Tyr Ala Lys Cys His Arg Gln Val Ile Arg Leu His Ile Ile  
 180 185 190  
 Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu Leu  
 195 200 205  
 Ile Phe Ser Leu Trp Thr Leu His Gln Arg Met Gln Gln His Val Gln  
 210 215 220  
 Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln Thr  
 225 230 235 240  
 Val Ile Ala Phe Phe Leu Leu Tyr Ser Ile Phe Ile Leu Ser Val Leu  
 245 250 255  
 Ile Gln Asn Glu Leu Leu Lys Lys Asn Leu Phe Val Val Phe Cys Glu  
 260 265 270  
 Val Val Tyr Ile Ala Phe Pro Thr Phe His Ser Tyr Ile Leu Ile Val  
 275 280 285  
 Gly Asp Met Lys Leu Arg Gln Ala Cys Leu Pro Leu Cys Ile Ile Ala  
 290 295 300  
 Ala Glu Ile Gln Thr Thr Leu Cys Arg Asn Phe Arg Ser Leu Lys Tyr  
 305 310 315 320  
 Phe Arg Leu Cys Cys Ile Phe  
 325

<210> 106

<211> 1374

<212> DNA

<213> Mus sp.

<220>

<223> mouse T2R01 (mGR01)

<400> 106

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ctgtgaaggc agagttacga aaaaaaatgt tatgagaacc aactcagaaa ttgacaaaaa 180
ttttctaaat gtcattttta aaaattatat ttcaaattgga aatgtgagca aatctttata 240
actaatatat aaaatgcagc atctttttaa gacaatattt gttatctgcc atagcacact 300
tgcaatcatt ttaatctttg aattaataat tggaatttta ggaaatgggt tcatggccct 360
ggtgcactgt atggactggg ttaagagaaa gaaaatgtcc ttagttaata aaatcctcac 420
tgctttggca atctccagaa tttttcatct cagttttattg cttataagtt tagtcatatt 480
cttttcatat tctgatattc ctatgacttc aaggatgaca caagtcagta ataatgtttg 540
  
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caagatatcc aattttttcta actctttttt tctttatcta aagtggagag ttgaaaaagt 660  
agtttcagtt acactgttgg tgtcattgct cctcctgatt ttaaataattt tattaattaa 720  
cttggaatt agcatatgca taaaggaatg tcaaagaaac atatcatgca gcttcagttc 780  
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ccccgttggt ttgtccctgt caacttttct cctgctcatc ttctccctgt ggacacttca 900  
ccagaggatg cagcagcatg ttcaggagg cagagatgcc agaaccacgg ccacttcaa 960  
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aatacaaata tgaattactg aagaaaaatc ttttcgttgt attttgtgag gttgtatata 1080  
tagcttttcc gacattccat tcatatattc tgattgtagg agacatgaag ctgagacagg 1140  
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gatcactaaa gtactttaga ttatgttgta tattctagac aaaaattaac tgatacaaat 1260  
gtcttttgta tttttcattt taaatatcct ttaattttga ctgcatgaaa ttgatttctg 1320  
cttgcaatta tcactgatta aaactattaa taatttaact agttgtatac aagg 1374

<210> 107  
<211> 327  
<212> PRT  
<213> Mus sp.

<220>  
<223> mouse T2R02 (mGR02)

<400> 107  
Met Glu Ser Val Leu His Asn Phe Ala Thr Val Leu Ile Tyr Val Glu  
1 5 10 15  
Phe Ile Phe Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ser Asn Phe  
20 25 30  
Leu Asp Trp Val Ile Lys Gln Lys Leu Ser Leu Ile Asp Lys Ile Leu  
35 40 45  
Leu Thr Leu Ala Ile Ser Arg Ile Thr Leu Ile Trp Glu Ile Tyr Ala  
50 55 60  
Trp Phe Lys Ser Leu Tyr Asp Pro Ser Ser Phe Leu Ile Gly Ile Glu  
65 70 75 80  
Phe Gln Ile Ile Tyr Phe Ser Trp Val Leu Ser Ser His Phe Ser Leu  
85 90 95  
Trp Leu Ala Thr Thr Leu Ser Val Phe Tyr Leu Leu Arg Ile Ala Asn  
100 105 110  
Cys Ser Trp Gln Ile Phe Leu Tyr Leu Lys Trp Arg Leu Lys Gln Leu  
115 120 125  
Ile Val Gly Met Leu Leu Gly Ser Leu Val Phe Leu Leu Gly Asn Leu  
130 135 140  
Met Gln Ser Met Leu Glu Glu Arg Phe Tyr Gln Tyr Gly Arg Asn Thr  
145 150 155 160  
Ser Val Asn Thr Met Ser Asn Asp Leu Ala Met Trp Thr Glu Leu Ile  
165 170 175  
Phe Phe Asn Met Ala Met Phe Ser Val Ile Pro Phe Thr Leu Ala Leu  
180 185 190

Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln Lys  
195 200 205

Met Gln Leu Ile Ser Arg Arg His Arg Asp Pro Ser Thr Lys Ala His  
210 215 220

Met Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu Tyr Thr Met  
225 230 235 240

His Phe Leu Ser Leu Leu Ile Ser Trp Ile Ala Gln Lys His Gln Ser  
245 250 255

Glu Leu Ala Asp Ile Ile Gly Met Ile Thr Glu Leu Met Tyr Pro Ser  
260 265 270

Val His Ser Cys Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr  
275 280 285

Ser Leu Cys Met Leu Arg His Leu Arg Cys Arg Leu Lys Gly Glu Asn  
290 295 300

Ile Thr Ile Ala Tyr Ser Asn Gln Ile Thr Ser Phe Cys Val Phe Cys  
305 310 315 320

Val Ala Asn Lys Ser Met Arg  
325

<210> 108  
<211> 1759  
<212> DNA  
<213> Mus sp.

<220>  
<223> mouse T2R02 (mGR02)

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gccaaagcttt ctatgaacat ggaatctgtc cttcacaact ttgccactgt actaatatac 120  
gtggagttaa tttttgggaa tttgagcaat ggattcatag tgttgtcaaa cttcttggac 180  
tgggtcatta aacaaaagct ttccttaata gataaaattc ttcttacatt ggcaatttca 240  
agaatcactc tcatctggga aatatatgct tggtttaaaa gtttatatga tccatcttcc 300  
tttttaattg gaatagaatt tcaaattatt tatttttagct gggtcctttc tagtcacttc 360  
agcctctggc ttgccacaac tctcagcgct ttttatttac tcagaatagc taactgctcc 420  
tggcagatct ttctctatct gaaatggaga cttaaacaac tgattgtggg gatgttgctg 480  
ggaagcttgg tgttcttgct tggaaatctg atgcaaagca tgcttgaaga gaggttctat 540  
caatatggaa ggaacacaag tgtgaatacc atgagcaatg accttgcaat tgggaccgag 600  
ctgatctttt tcaacatggc tatgttctct gtaataccat ttacattggc cttgatttct 660  
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agacacagag accctagcac caaggcccac atgaatgcct tgagaattat ggtgtccttc 780  
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cagagtgaac tggctgatat tattggtatg ataactgaac tcatgtatcc ttcagtccat 900  
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catttgagat gtaggctgaa aggagagaat atcacaattg catatagcaa ccaaataact 1020  
agcttttgtg tattctgtgt tgcaaacaaa tctatgaggt agttgttcaa ggaatccttc 1080  
cttgacttat tgtatcatgg aagtcatatg ggggagctgt aaagagctgt cttctgtaag 1140  
caaggtttgt atacactagt ggggctggga caccaacca agcacaaaac ctagctataa 1200  
cctatcctgg ctgcaggata tgcagggaaca atggtggcct ggaaattgtg ggactggcaa 1260  
agcaatagct agtctaactt gaggccatt ccacagcagg aagctcatgc ccacctctgc 1320  
ctggatggcc aggaagcaaa atcttgatgg cccaagacc tatggtaaac tgaacactac 1380  
tggaaaaaga aagactcgtg ttaatgatct atcaaatatt tcctaataat attctgataa 1440

actcatatat tagtccctgt cctaatacatc atcactggga ctccttccca gcacctgatg 1500  
 ggagcagata gagatctaca tccaaatagt aagtgtatct tggggaactc cacttaagaa 1560  
 tagaaggaac aattatgaga gccagagtga tccagaacac taggatcaca gaatcaacta 1620  
 agcagcatgc ataggggtta atggagactg aagtggcaat cacagagcct gcataggtct 1680  
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 aacaatggat aaggaattc 1759

<210> 109  
 <211> 312  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R03 (mGR03)

<400> 109  
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 Ile Ser Leu Glu Phe Ile Ile Gly Ile Leu Gly Asn Val Phe Ile Ala  
 20 25 30  
 Leu Val Asn Ile Ile Asp Trp Val Lys Arg Gly Lys Ile Ser Ala Val  
 35 40 45  
 Asp Lys Thr Tyr Met Ala Leu Ala Ile Ser Arg Thr Ala Phe Leu Leu  
 50 55 60  
 Ser Leu Ile Thr Gly Phe Leu Val Ser Leu Leu Asp Pro Ala Leu Leu  
 65 70 75 80  
 Gly Met Arg Thr Met Val Arg Leu Leu Thr Ile Ser Trp Met Val Thr  
 85 90 95  
 Asn His Phe Ser Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe  
 100 105 110  
 Leu Lys Ile Ala Asn Phe Ser Asn Ser Ile Phe Leu Val Leu Lys Trp  
 115 120 125  
 Glu Ala Lys Lys Val Val Ser Val Thr Leu Val Val Ser Val Ile Ile  
 130 135 140  
 Leu Ile Met Asn Ile Ile Val Ile Asn Lys Phe Thr Asp Arg Leu Gln  
 145 150 155 160  
 Val Asn Thr Leu Gln Asn Cys Ser Thr Ser Asn Thr Leu Lys Asp Tyr  
 165 170 175  
 Gly Leu Phe Leu Phe Ile Ser Thr Gly Phe Thr Leu Thr Pro Phe Ala  
 180 185 190  
 Val Ser Leu Thr Met Phe Leu Leu Ile Phe Ser Leu Trp Arg His  
 195 200 205  
 Leu Lys Asn Met Cys His Ser Ala Thr Gly Ser Arg Asp Val Ser Thr  
 210 215 220  
 Val Ala His Ile Lys Gly Leu Gln Thr Val Val Thr Phe Leu Leu Leu  
 225 230 235 240

Tyr Thr Ala Phe Val Met Ser Leu Leu Ser Glu Ser Leu Asn Ile Asn  
                     245                    250                    255  
 Ile Gln His Thr Asn Leu Leu Ser His Phe Leu Arg Ser Ile Gly Val  
                     260                    265                    270  
 Ala Phe Pro Thr Gly His Ser Cys Val Leu Ile Leu Gly Asn Ser Lys  
                     275                    280                    285  
 Leu Arg Gln Ala Ser Leu Ser Val Ile Leu Trp Leu Arg Tyr Lys Tyr  
                     290                    295                    300  
 Lys His Ile Glu Asn Trp Gly Pro  
 305                    310

<210> 110  
 <211> 1484  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R03 (mGR03)

<400> 110  
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 gactgctgta tacagggcat gaagcatctg gatgaagttc agctgtgctg cctttgacaa 120  
 caatttttttg tgtatgtgtg gagaacataa accatttcat tagtgaaatt tggccttttgg 180  
 gtgacattgt ctatgatagt tctgaaagtg attatgttaa gaatcagaca cagccgtcta 240  
 gaagattgta ttaacacatc tttggtagtt cagaagaaat tagatcatca tgggtgttgac 300  
 aataagggct attttatggg taacattgat aactattata agtctggagt ttatcatagg 360  
 aatttttagga aatgtattca tagctctcgt gaacatcata gactgggtta aaagaggaaa 420  
 gatctctgca gtggataaga cctatatggc cctggccatc tccaggactg cttttttatt 480  
 gtcactaatc acaggggttct tgggtatcatt attggacca gctttatttg gaatgagaac 540  
 gatggtaagg ctcccttacta tttcctggat ggtgaccaat catttcagt tctgggttgc 600  
 aacatgcctc agtatctttt attttctcaa gatagctaatt ttctcaaatt ctattttcct 660  
 tgttctcaaa tgggaagcta aaaaagtggt atcagtgaca ttggtggtat ctgtgataat 720  
 cttgatcatg aacattatag tcataaaca attcactgac agacttcaag taaacacact 780  
 ccagaactgt agtacaagta acactttaaa agattatggg ctctttttat tcattagcac 840  
 tgggttttaca ctaccccat tcgctgtgtc tttgacaatg tttcttctgc tcatcttctc 900  
 cctgtggaga catctgaaga atatgtgtca cagtgccaca ggctccagag atgtcagcac 960  
 agtggcccac ataaaaggct tgcaaactgt ggtaaccttc ctgttactat atactgcttt 1020  
 tgttatgtca cttctttcag agtctttgaa tattaacatt caacatacaa atcttctttc 1080  
 tcatttttta cggagtatag gagtagcttt tcccacaggc cactcctgtg tactgattct 1140  
 tggaaacagt aagctgaggc aagcctctct ttctgtgata ttgtggctga ggtataagta 1200  
 caaacatata gagaattggg gcccctaaat catatcaggg atccttttcc acattctaga 1260  
 aaaaaatcag ttaataagaa caggaattta ggaaggaatc tgaaattatg aatctcatag 1320  
 gccatgaacc ttcagacaaa ggattcatta gagagataga gagagaacat tgttatctgt 1380  
 aactcgacag gcaacactgt agattatgaa aataaatgtc agtctgtaat ggaaagcaaa 1440  
 acatgctata ttttattaat tggttttggt ttaaggtcgg gata 1484

<210> 111  
 <211> 302  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R04 (mGR04)

<400> 111

Met	Leu	Ser	Ala	Leu	Glu	Ser	Ile	Leu	Leu	Ser	Val	Ala	Thr	Ser	Glu
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Ala	Met	Leu	Gly	Val	Leu	Gly	Asn	Thr	Phe	Ile	Val	Leu	Val	Asn	Tyr
			20					25					30		
Thr	Asp	Trp	Val	Arg	Asn	Lys	Lys	Leu	Ser	Lys	Ile	Asn	Phe	Ile	Leu
		35					40					45			
Thr	Gly	Leu	Ala	Ile	Ser	Arg	Ile	Phe	Thr	Ile	Trp	Ile	Ile	Thr	Leu
	50					55					60				
Asp	Ala	Tyr	Thr	Lys	Val	Phe	Leu	Leu	Thr	Met	Leu	Met	Pro	Ser	Ser
65					70					75					80
Leu	His	Glu	Cys	Met	Ser	Tyr	Ile	Trp	Val	Ile	Ile	Asn	His	Leu	Ser
				85					90					95	
Val	Trp	Phe	Ser	Thr	Ser	Leu	Gly	Ile	Phe	Tyr	Phe	Leu	Lys	Ile	Ala
			100					105					110		
Asn	Phe	Ser	His	Tyr	Ile	Phe	Leu	Trp	Met	Lys	Arg	Arg	Ala	Asp	Lys
		115					120					125			
Val	Phe	Val	Phe	Leu	Ile	Val	Phe	Leu	Ile	Ile	Thr	Trp	Leu	Ala	Ser
	130					135					140				
Phe	Pro	Leu	Ala	Val	Lys	Val	Ile	Lys	Asp	Val	Lys	Ile	Tyr	Gln	Ser
145					150					155					160
Asn	Thr	Ser	Trp	Leu	Ile	His	Leu	Glu	Lys	Ser	Glu	Leu	Leu	Ile	Asn
				165					170					175	
Tyr	Val	Phe	Ala	Asn	Met	Gly	Pro	Ile	Ser	Leu	Phe	Ile	Val	Ala	Ile
			180					185					190		
Ile	Ala	Cys	Phe	Leu	Leu	Thr	Ile	Ser	Leu	Trp	Arg	His	Ser	Arg	Gln
		195					200					205			
Met	Gln	Ser	Ile	Gly	Ser	Gly	Phe	Arg	Asp	Leu	Asn	Thr	Glu	Ala	His
	210					215					220				
Met	Lys	Ala	Met	Lys	Val	Leu	Ile	Ala	Phe	Ile	Ile	Leu	Phe	Ile	Leu
225					230					235					240
Tyr	Phe	Leu	Gly	Ile	Leu	Ile	Glu	Thr	Leu	Cys	Leu	Phe	Leu	Thr	Asn
				245					250					255	
Asn	Lys	Leu	Leu	Phe	Ile	Phe	Gly	Phe	Thr	Leu	Ser	Ala	Met	Tyr	Pro
			260					265						270	
Cys	Cys	His	Ser	Phe	Ile	Leu	Ile	Leu	Thr	Ser	Arg	Glu	Leu	Lys	Gln
		275					280					285			
Asp	Thr	Met	Arg	Ala	Leu	Gln	Arg	Leu	Lys	Cys	Cys	Glu	Thr		
	290					295					300				

<210> 112  
 <211> 1529  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R04 (mGR04)

<400> 112  
 ctgcagcagg taaatcacac cagatccagc agaagccttc ttggaaattg gcagagatgc 60  
 tgagtgcact ggaaagcatc ctcccttctg ttgccactag tgaagccatg ctgggagttt 120  
 tagggaacac atttattgta cttgtaaaact acacagactg ggtcaggaat aagaaactct 180  
 ctaagattaa ctttattctc actggcttag caatttccag gatttttacc atatggataa 240  
 taacttttaga tgcataatac aagggttttc ttctgactat gcttatgccg agcagtctac 300  
 atgaatgcat gagttacata tgggtaatta ttaaccatct gagcgttttg tttagcacca 360  
 gcctcggcat cttttatttt ctgaagatag caaatttttc ccactacata tttctctgga 420  
 tgaagagaag agctgataaa gtttttgtct ttctaattgt attcttaatt ataacgtggc 480  
 tagcttcctt tccgctagct gtgaagggtca ttaaagatgt taaaatatat cagagcaaca 540  
 catcctggct gatccacctg gagaagagtg agttacttat aaactatgtt tttgccaata 600  
 tggggcccat ttccctcttt attgtagcca taattgcttg tttcttgta accatttccc 660  
 tttggagaca cagcaggcag atgcaatcca ttggatcagg attcagagat ctcaacacag 720  
 aagctcacat gaaagccatg aaagttttaa ttgcatttat catcctcttt atcttatatt 780  
 ttttgggtat tctcatagaa acattatgct tgtttcttac aaacaataaa cttctcttta 840  
 tttttggctt cactttgtca gccatgtatc cctgttgcca ttccctttatc ctaattctaa 900  
 caagcaggga gctgaagcaa gacactatga gggcactgca gagattaaaa tgctgtgaga 960  
 cttgacagag aaatgaatgt tctggcacag ttcagcaggg aatccctgga gccctttcca 1020  
 ttccactat gttctcacac tgtctttagt tgaattgtta aaagttttg aaacctttgg 1080  
 caactgattg actgcagcta cgccagtgtg agattttcat agtaagagca aacattgaaa 1140  
 ataagacttc tcagtcttat ttcattgagt ttctaaagca ttgacaccca ttcaccagaa 1200  
 aaaccaaagg ggaagagagg agttttcaga catgtgtgat gaatcttgat atttaggaca 1260  
 tgggaattgag gagccagagg gatgctaccg tgtgtctaca gctttgtttg ttaaatagct 1320  
 acttttcctt tcccagttag ttaaagtaga tgcttggagt agtggtgaaa atcatggcag 1380  
 tagatgggat ctgtgggaag tggttgagga agcaggctgt ttctgaacga agagaccaga 1440  
 ggactgattg aactgggtcat tgtgtatatc aaaaatagtg atttcagatg aagccaagtt 1500  
 gtagagcaaa gatattctgag gaagaattc 1529

<210> 113  
 <211> 300  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R05 (mGR05)

<400> 113  
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 1 5 10 15  
 Ala Gly Leu Gly Val Leu Gly Asn Thr Phe Ile Ala Leu Val Asn Cys  
 20 25 30  
 Met Asp Trp Ala Lys Asn Asn Lys Leu Ser Met Thr Gly Phe Leu Leu  
 35 40 45  
 Ile Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Leu Leu Thr Leu  
 50 55 60  
 Asp Ala Tyr Ala Lys Leu Phe Tyr Pro Ser Lys Tyr Phe Ser Ser Ser  
 65 70 75 80

Leu Ile Glu Ile Ile Ser Tyr Ile Trp Met Thr Val Asn His Leu Thr  
                             85                            90                            95  
 Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala  
                             100                            105                            110  
 Asn Phe Ser Asp Cys Val Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys  
                             115                            120                            125  
 Ala Phe Val Phe Leu Leu Gly Cys Leu Leu Thr Ser Trp Val Ile Ser  
                             130                            135                            140  
 Phe Ser Phe Val Val Lys Val Met Lys Asp Gly Lys Val Asn His Arg  
                             145                            150                            155                            160  
 Asn Arg Thr Ser Glu Met Tyr Trp Glu Lys Arg Gln Phe Thr Ile Asn  
                             165                            170                            175  
 Tyr Val Phe Leu Asn Ile Gly Val Ile Ser Leu Phe Met Met Thr Leu  
                             180                            185                            190  
 Thr Ala Cys Phe Leu Leu Ile Met Ser Leu Trp Arg His Ser Arg Gln  
                             195                            200                            205  
 Met Gln Ser Gly Val Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His  
                             210                            215                            220  
 Val Lys Ala Ile Lys Phe Leu Ile Ser Phe Ile Ile Leu Phe Val Leu  
                             225                            230                            235                            240  
 Tyr Phe Ile Gly Val Ser Ile Glu Ile Ile Cys Ile Phe Ile Pro Glu  
                             245                            250                            255  
 Asn Lys Leu Leu Phe Ile Phe Gly Phe Thr Thr Ala Ser Ile Tyr Pro  
                             260                            265                            270  
 Cys Cys His Ser Phe Ile Leu Ile Leu Ser Asn Ser Gln Leu Lys Gln  
                             275                            280                            285  
 Ala Phe Val Lys Val Leu Gln Gly Leu Lys Phe Phe  
                             290                            295                            300

<210> 114

<211> 903

<212> DNA

<213> Mus sp.

<220>

<223> mouse T2R05 (mGR05)

<400> 114

atgctgagtg cggcagaagg catcctcctt tccattgcaa ctggtgaagc tgggctggga 60  
 gtttttaggga acacatttat tgcactggta aactgcatgg actgggcca gaacaataag 120  
 ctttctatga ctggcttcct tctcatcggc ttagcaactt ccaggatttt tatttgtgtg 180  
 ctattaactt tagatgcata tgcaaagcta ttctatccaa gtaagtattt ttctagtagt 240  
 ctgattgaaa tcatctctta tatatggatg actgtgaatc acctgactgt ctggtttgcc 300  
 accagcctaa gcatcttcta tttcctgaag atagccaatt tttccgactg tgtatttctc 360  
 tgggtgaaga ggagaactga taaagctttt gtttttctct tggggtggtt gctaacttca 420  
 tgggtaatct ccttctcatt tggtgtgaag gtgatgaagg acggtaaagt gaatcataga 480  
 aacaggacct cggagatgta ctgggagaaa aggcaattca ctattaacta cgttttcctc 540

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aatattggag tcatttctct ctttatgatg accttaactg catgtttctt gttaattatg 600
tcactttgga gacacagcag gcagatgcag tctggtgttt caggattcag agacctcaac 660
acagaagctc atgtgaaagc cataaaattt ttaatttcat ttatcatcct ttctgtcttg 720
tattttatag gtgtttcaat agaaaattatc tgcataattta taccagaaaa caaactgcta 780
tttatttttg gtttcacaac tgcattccata tatccttgct gtcactcatt tattctaatt 840
ctatctaaca gccagctaaa gcaagccttt gtaaagggtac tgcaaggatt aaagttcttt 900
tag 903

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<210> 115  
 <211> 308  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R06 (mGR06)

<400> 115  
 Met Leu Thr Val Ala Glu Gly Ile Leu Leu Cys Phe Val Thr Ser Gly  
 1 5 10 15  
 Ser Val Leu Gly Val Leu Gly Asn Gly Phe Ile Leu His Ala Asn Tyr  
 20 25 30  
 Ile Asn Cys Val Arg Lys Lys Phe Ser Thr Ala Gly Phe Ile Leu Thr  
 35 40 45  
 Gly Leu Ala Ile Cys Arg Ile Phe Val Ile Cys Ile Ile Ile Ser Asp  
 50 55 60  
 Gly Tyr Leu Lys Leu Phe Ser Pro His Met Val Ala Ser Asp Ala His  
 65 70 75 80  
 Ile Ile Val Ile Ser Tyr Ile Trp Val Ile Ile Asn His Thr Ser Ile  
 85 90 95  
 Trp Phe Ala Thr Ser Leu Asn Leu Phe Tyr Leu Leu Lys Ile Ala Asn  
 100 105 110  
 Phe Ser His Tyr Ile Phe Phe Cys Leu Lys Arg Arg Ile Asn Thr Val  
 115 120 125  
 Phe Ile Phe Leu Leu Gly Cys Leu Phe Ile Ser Trp Ser Ile Ala Phe  
 130 135 140  
 Pro Gln Thr Val Lys Ile Phe Asn Val Lys Lys Gln His Arg Asn Val  
 145 150 155 160  
 Ser Trp Gln Val Tyr Leu Tyr Lys Asn Glu Phe Ile Val Ser His Ile  
 165 170 175  
 Leu Leu Asn Leu Gly Val Ile Phe Phe Phe Met Val Ala Ile Ile Thr  
 180 185 190  
 Cys Phe Leu Leu Ile Ile Ser Leu Trp Lys His Asn Arg Lys Met Gln  
 195 200 205  
 Leu Tyr Ala Ser Arg Phe Lys Ser Leu Asn Thr Glu Val His Val Lys  
 210 215 220



Val Met Lys Val Leu Ile Ser Phe Ile Ile Leu Leu Ile Leu His Phe  
 225 230 235 240

Ile Gly Ile Leu Ile Glu Thr Leu Ser Phe Leu Lys Tyr Glu Asn Lys  
 245 250 255

Leu Leu Leu Ile Leu Gly Leu Ile Ile Ser Cys Met Tyr Pro Cys Cys  
 260 265 270

His Ser Phe Ile Leu Ile Leu Ala Asn Ser Gln Leu Lys Gln Ala Ser  
 275 280 285

Leu Lys Ala Leu Lys Gln Leu Lys Cys His Lys Lys Asp Lys Asp Val  
 290 295 300

Arg Val Thr Trp  
 305

<210> 116  
 <211> 1242  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R06 (mGR06)

<400> 116  
 tatagttgca gcagaagcaa cgttagggat ctgtagagat gctgactgta gcagaaggaa 60  
 tcctcctttg ttttgtaact agtggttcag tcctgggagt tctaggaaat ggatttatcc 120  
 tgcattgcaa ctacattaac tgtgtcagaa agaagttctc cacagctggc tttattctca 180  
 caggcttggc tatttgcaga atctttgtca tatgtataat aatctctgat ggatatttaa 240  
 aattgttttc tccacatatg gttgcctctg atgcccacat tatagtgatt tcttacatat 300  
 gggtaattat caatcataca agtatatggt ttgccaccag cctcaacctc ttctatctcc 360  
 tgaagatagc aaatttttct cactacatct tcttctgctt gaagagaaga atcaatacag 420  
 tatttatctt tctcctggga tgcttattta tatcatgggc aattgctttc ccacaaacag 480  
 tgaagatatt taatgttaaa aagcagcaca gaaatgtttc ctggcagggtt tacctctata 540  
 agaatgagtt cattgtaagc cacattcttc tcaacctggg agttatatcc ttctttatgg 600  
 tggctatcat tacatgcttc ctattaatta tttcactttg gaaacataac agaaagatgc 660  
 agttgtatgc ctcaagattc aaaagcctta acacagaagt acatgtgaaa gtcatagaaag 720  
 ttttaatttc ttttattatc ctgttaattc tgcatttcat agggattttg atagaaacat 780  
 tgagcttttt aaaatatgaa aataaaactgc tacttatttt gggtttgata atttcatgca 840  
 tgtatccttg ctgtcattca tttatcctaa ttctagcaaa cagtcagctg aagcaggctt 900  
 ctttgaaggc actgaagcaa ttaaaatgcc ataagaaaga caaggacgtc agagtgcacat 960  
 ggtagactta tggagaaatg aatgggcaca agaaatagcc tgggtgtggag atgttgatat 1020  
 ctctaaagac cgtttcactt ccaaattctt gcaattattt aaaaaaaaaa gtcttgctga 1080  
 tatcatggaa tcatgggaaa tggtgcaatt gtgttttggg gacagggtga ccagtgaagg 1140  
 tatggttaag cagcgaaaca ctcatacagc tcgttcgttc tttttgtatt ttattttgtg 1200  
 ttggtggcct tccaagacat gatttctcta tgtaagtttt gg 1242

<210> 117  
 <211> 308  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R07 (mGR07)

<400> 117

Met Leu Asn Ser Ala Glu Gly Ile Leu Leu Cys Val Val Thr Ser Glu  
1 5 10 15  
Ala Val Leu Gly Val Leu Gly Asp Thr Tyr Ile Ala Leu Phe Asn Cys  
20 25 30  
Met Asp Tyr Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Ile Leu  
35 40 45  
Ile Gly Leu Ala Ile Ser Arg Ile Gly Val Val Trp Ile Ile Ile Leu  
50 55 60  
Gln Gly Tyr Ile Gln Val Phe Phe Pro His Met Leu Thr Ser Gly Asn  
65 70 75 80  
Ile Thr Glu Tyr Ile Thr Tyr Ile Trp Val Phe Leu Asn His Leu Ser  
85 90 95  
Val Trp Phe Val Thr Asn Leu Asn Ile Leu Tyr Phe Leu Lys Ile Ala  
100 105 110  
Asn Phe Ser Asn Ser Val Phe Leu Trp Leu Lys Arg Arg Val Asn Ala  
115 120 125  
Val Phe Ile Phe Leu Ser Gly Cys Leu Leu Thr Ser Trp Leu Leu Cys  
130 135 140  
Phe Pro Gln Met Thr Lys Ile Leu Gln Asn Ser Lys Met His Gln Arg  
145 150 155 160  
Asn Thr Ser Trp Val His Gln Arg Lys Asn Tyr Phe Leu Ile Asn Gln  
165 170 175  
Ser Val Thr Asn Leu Gly Ile Phe Phe Phe Ile Ile Val Ser Leu Ile  
180 185 190  
Thr Cys Phe Leu Leu Ile Val Phe Leu Trp Arg His Val Arg Gln Met  
195 200 205  
His Ser Asp Val Ser Gly Phe Arg Asp His Ser Thr Lys Val His Val  
210 215 220  
Lys Ala Met Lys Phe Leu Ile Ser Phe Met Val Phe Phe Ile Leu His  
225 230 235 240  
Phe Val Gly Leu Ser Ile Glu Val Leu Cys Phe Ile Leu Pro Gln Asn  
245 250 255  
Lys Leu Leu Phe Ile Thr Gly Leu Thr Ala Thr Cys Leu Tyr Pro Cys  
260 265 270  
Gly His Ser Ile Ile Val Ile Leu Gly Asn Lys Gln Leu Lys Gln Ala  
275 280 285  
Ser Leu Lys Ala Leu Gln Gln Leu Lys Cys Cys Glu Thr Lys Gly Asn  
290 295 300  
Phe Arg Val Lys  
305

<210> 118  
 <211> 1754  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R07 (mGR07)

<400> 118  
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 agtgatacta cacatttgat tgctaaatgc aaatagttcc aaaggaacaa gtaaatttta 120  
 tgaaatagaa gcttctatatt gcttattaac aaactgcaag caaacattag tctgcacaca 180  
 ttttatagac aagctaaatc ttcaaaagca ataaaaaaga gcaccataa agttctgact 240  
 ctatcacatg acaataggct tgaaaagatt gtctatgtag ataaagaaga tggcataact 300  
 tctccatcaa gaagccagta tatgggacat tctccagcag ataatttaca atagatgcag 360  
 cagaagtaac cttagagatc tgtaaagatg ctgaattcag cagaaggcat cctcctttgt 420  
 gttgtcacta gtgaggctgt gctcggaggt ttaggggaca catatattgc acttttttaac 480  
 tgcattggact atgctaagaa caagaagctc tctaagatcg gtttcattct cattggcctg 540  
 gcgatttcca gaattggtgt tgtatggata ataattttac aagggtatat acaagtattt 600  
 tttccacaca tgcttacctc tggaaacata actgaatata ttacttacat atgggtattt 660  
 ctcaatcact taagtgtctg gtttgtcacc aacctcaaca tctctactt tctaaagata 720  
 gctaattttt ccaactctgt atttctctgg ctgaaaagga gagtcaatgc agtttttatc 780  
 tttctgtcag gatgcttact tacctcatgg ttactatggt ttccacaaat gacaaagata 840  
 cttcaaaata gtaaaatgca ccagagaaac acatcttggg tccaccagcg gaaaaattac 900  
 tttcttatta accaaagtgt gaccaatctg ggaatctttt tcttcattat tgtatccctg 960  
 attacctgct ttctgttgat tgttttcctc tggagacatg tcagacaaat gcactcagat 1020  
 gtttcaggat tcagagacca cagcacaaaa gtacatgtga aagctatgaa attttctaata 1080  
 tcttttatgg tcttctttat tctgcatttt gtaggccttt ccatagaagt gctatgcttt 1140  
 attctgccac aaaataaact gctctttata actggtttga cagccacatg cctctatccc 1200  
 tgcggtcact caatcatcgt aatttttagga aataagcagt taaagcaagc ctctttgaag 1260  
 gcactgcagc aactaaaatg ctgtgagaca aaaggaaatt tcagagtcaa ataaatgggt 1320  
 ttgcaaaata atagctgcct tgttcttcca ctggttttta ccctgttagt tgatgttatg 1380  
 aaaagttcct gctatgggtg atgacatctc aaggaaatcta tttttctggt ggcatgttaa 1440  
 gtccacgtga agcctcactt catactgtga cttgactatg caaattcttt ccacaaaata 1500  
 accagataac attcagcctg gagataaatt catttaaagg cttttatggt gaggataaac 1560  
 aaaaaaaaaa aatcattttt ctgtgattca ctgtaactcc caggatgagt aaaagaaaac 1620  
 aagacaaatg gttgtgatca gcctttgtgt gtctagacag agctagggag cagatgttga 1680  
 tgcttggtgt tgggttttag ttctttaaga agttattgcc tctctgccat tcggtattcc 1740  
 tcaggtgaga attc 1754

<210> 119  
 <211> 297  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R08 (mGR08)

<400> 119  
 Met Leu Trp Glu Leu Tyr Val Phe Val Phe Ala Ala Ser Val Phe Leu  
 1 5 10 15  
 Asn Phe Val Gly Ile Ile Ala Asn Leu Phe Ile Ile Val Ile Ile Ile  
 20 25 30  
 Lys Thr Trp Val Asn Ser Arg Arg Ile Ala Ser Pro Asp Arg Ile Leu  
 35 40 45  
 Phe Ser Leu Ala Ile Thr Arg Phe Leu Thr Leu Gly Leu Phe Leu Leu  
 50 55 60

Asn Ser Val Tyr Ile Ala Thr Asn Thr Gly Arg Ser Val Tyr Phe Ser  
 65 70 75 80  
 Thr Phe Phe Leu Leu Cys Trp Lys Phe Leu Asp Ala Asn Ser Leu Trp  
 85 90 95  
 Leu Val Thr Ile Leu Asn Ser Leu Tyr Cys Val Lys Ile Thr Asn Phe  
 100 105 110  
 Gln His Pro Val Phe Leu Leu Leu Lys Arg Thr Ile Ser Met Lys Thr  
 115 120 125  
 Thr Ser Leu Leu Leu Ala Cys Leu Leu Ile Ser Ala Leu Thr Thr Leu  
 130 135 140  
 Leu Tyr Tyr Met Leu Ser Gln Ile Ser Arg Phe Pro Glu His Ile Ile  
 145 150 155 160  
 Gly Arg Asn Asp Thr Ser Phe Asp Leu Ser Asp Gly Ile Leu Thr Leu  
 165 170 175  
 Val Ala Ser Leu Val Leu Asn Ser Leu Leu Gln Phe Met Leu Asn Val  
 180 185 190  
 Thr Phe Ala Ser Leu Leu Ile His Ser Leu Arg Arg His Ile Gln Lys  
 195 200 205  
 Met Gln Arg Asn Arg Thr Ser Phe Trp Asn Pro Gln Thr Glu Ala His  
 210 215 220  
 Met Gly Ala Met Arg Leu Met Ile Cys Phe Leu Val Leu Tyr Ile Pro  
 225 230 235 240  
 Tyr Ser Ile Ala Thr Leu Leu Tyr Leu Pro Ser Tyr Met Arg Lys Asn  
 245 250 255  
 Leu Arg Ala Gln Ala Ile Cys Met Ile Ile Thr Ala Ala Tyr Pro Pro  
 260 265 270  
 Gly His Ser Val Leu Leu Ile Ile Thr His His Lys Leu Lys Ala Lys  
 275 280 285  
 Ala Lys Lys Ile Phe Cys Phe Tyr Lys  
 290 295

<210> 120  
 <211> 1475  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R08 (mGR08)

<400> 120  
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 ttgcatgc tggaaaataa aaaggagacc tctttccagg ctgcatcctg tgtctgctta 180  
 cttatttcag tttgttttca tcggcaccaa acgaggaaag atgctctggg aactgtatgt 240  
 atttgtgtt gctgcctcgg ttttttttaa tttgttagga atcattgcaa atctatttat 300  
 tatagtata attattaaga cttgggtcaa cagtcgcaga attgcctctc cggataggat 360

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cctgttcagc ttggccatca ctagattcct gactttgggg ttgtttctac tgaacagtgt 420
ctacattgct acaaatactg gaagggtcagt ctacttttcc acattttttc tattgtgttg 480
gaagtttctg gatgcaaaca gtctctggtt agtgaccatt ctgaacagct tgtattgtgt 540
gaagattact aattttcaac acccagtggt tctcctggtg aaacggacta tctctatgaa 600
gaccaccagc ctgctgttgg cctgtcttct gatttcagcc ctcaccactc tcctatatta 660
tatgctctca cagatatcac gttttcctga acacataatt gggagaaatg acacgtcatt 720
tgacctcagt gatggtatct tgacgttagt agcctctttg gtcctgaact cacttctaca 780
gtttatgctc aatgtgactt ttgcttcctt gttaatacat tccttgagaa gacatatata 840
gaagatgcag agaaacagga ccagcttttg gaatccccag acggagggtc acatgggtgc 900
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tcaattcatg gtttggttgc attagaaatg tctcagtgat ctaaggactt aattttgtga 1200
tcttgatctc ggcattcctga ccctgagact aagtgcctat attttggtca atacagcatc 1260
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atttttcatg gctatcacat tcctagacaa tggaaatcac catactgttt cgctagctac 1380
tgaagtacca ggggaaagtc catgaatgaa ggccacattg tgatgttctt ggtagcaca 1440
gattagagaa tttggcctca actgagcaag atatc 1475

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<210> 121  
 <211> 316  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R09 (mGR09)

<400> 121  
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 Leu Ile Ile Leu Phe Ile Glu Leu Ile Ile Gly Leu Ile Gly Asn Gly  
 20 25 30  
 Phe Thr Ala Leu Val His Cys Met Asp Trp Val Lys Arg Lys Lys Met  
 35 40 45  
 Ser Leu Val Asn Lys Ile Leu Thr Ala Leu Ala Thr Ser Arg Ile Phe  
 50 55 60  
 Leu Leu Trp Phe Met Leu Val Gly Phe Pro Ile Ser Ser Leu Tyr Pro  
 65 70 75 80  
 Tyr Leu Val Thr Thr Arg Leu Met Ile Gln Phe Thr Ser Thr Leu Trp  
 85 90 95  
 Thr Ile Ala Asn His Ile Ser Val Trp Phe Ala Thr Cys Leu Ser Val  
 100 105 110  
 Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Pro Phe Leu Tyr  
 115 120 125  
 Leu Lys Arg Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser  
 130 135 140  
 Leu Val Leu Leu Phe Leu Asn Ile Leu Leu Leu Asn Leu Glu Ile Asn  
 145 150 155 160

Met Cys Ile Asn Glu Tyr His Gln Ile Asn Ile Ser Tyr Ile Phe Ile  
165 170 175

Ser Tyr Tyr His Leu Ser Cys Gln Ile Gln Val Leu Gly Ser His Ile  
180 185 190

Ile Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu  
195 200 205

Leu Ile Phe Ser Leu Trp Thr Leu His Lys Arg Met Gln Gln His Val  
210 215 220

Gln Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln  
225 230 235 240

Ala Val Ile Ala Phe Leu Leu Leu Tyr Ser Ile Phe Ile Leu Ser Leu  
245 250 255

Leu Leu Gln Phe Trp Ile His Gly Leu Arg Lys Lys Pro Pro Phe Ile  
260 265 270

Ala Phe Cys Gln Val Val Asp Thr Ala Phe Pro Ser Phe His Ser Tyr  
275 280 285

Val Leu Ile Leu Arg Asp Arg Lys Leu Arg His Ala Ser Leu Ser Val  
290 295 300

Leu Ser Trp Leu Lys Cys Arg Pro Asn Tyr Val Lys  
305 310 315

<210> 122  
<211> 1339  
<212> DNA  
<213> Mus sp.

<220>  
<223> mouse T2R09 (mGR09)

<400> 122  
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tgatatcacc gagaacatac ttctaattat ttatttcatt gaattaataa ttggacttat 180  
aggaaacgga ttcacagcct tgggtgcactg catggactgg gttaagagaa aaaaaatgtc 240  
attagttaat aaaatcctca ccgctttggc aacttctaga attttcctgc tctgggtcat 300  
gctagtaggt tttccaatta gtcactgta cccatattta gttactacta gactgatgat 360  
acagttcact agtactctat ggactatagc taaccatatt agtgtctggt ttgctacatg 420  
cctcagtgtc ttttattttc tcaagatagc caatttttct aattctcctt ttctctatct 480  
aaagaggaga gttgaaaaag tagtttcagt tacattactg gtgtctctgg tcctcttggt 540  
tttaaatatt ttactactta atttggaat taacatgtgt ataaatgaat atcatcaaat 600  
aaacatatca tacatcttca tttcttatta ccatttaagt tgtcaaatc aggtgttagg 660  
aagtcacatt attttcctgt ctgtccccgt tgttttgtcc ctgtcaactt ttctcctgct 720  
catcttctcc ctgtggacac ttcacaagag gatgcagcag catgttcagg gaggcagaga 780  
tgccagaacc acggccact tcaaagcctt gcaagcagtg attgcctttc tcctactata 840  
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tcctttcatt gcattttgtc aggttgtaga tacagctttt ccttcattcc attcatatgt 960  
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attactaatt tagcaagtcg tatacaagggt tattttttta tacacatatc aaaaactgac 1200  
atgtttatgt tctacaaaaa cctgaatata tcaaaattat ataaattttg tatcaacgat 1260

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 gatgaaagtc tgaaagctt 1339

<210> 123  
 <211> 333  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R10 (mGR10)

<400> 123

Met	Phe	Ser	Gln	Ile	Ile	Ser	Thr	Ser	Asp	Ile	Phe	Thr	Phe	Thr	Ile	1	5	10	15
Ile	Leu	Phe	Val	Glu	Leu	Val	Ile	Gly	Ile	Leu	Gly	Asn	Gly	Phe	Ile	20	25	30	
Ala	Leu	Val	Asn	Ile	Met	Asp	Trp	Thr	Lys	Arg	Arg	Ser	Ile	Ser	Ser	35	40	45	
Ala	Asp	Gln	Ile	Leu	Thr	Ala	Leu	Ala	Ile	Thr	Arg	Phe	Leu	Tyr	Val	50	55	60	
Trp	Phe	Met	Ile	Ile	Cys	Ile	Leu	Leu	Phe	Met	Leu	Cys	Pro	His	Leu	65	70	75	80
Leu	Thr	Arg	Ser	Glu	Ile	Val	Thr	Ser	Ile	Gly	Ile	Ile	Trp	Ile	Val	85	90	95	
Asn	Asn	His	Phe	Ser	Val	Trp	Leu	Ala	Thr	Cys	Leu	Gly	Val	Phe	Tyr	100	105	110	
Phe	Leu	Lys	Ile	Ala	Asn	Phe	Ser	Asn	Ser	Leu	Phe	Leu	Tyr	Leu	Lys	115	120	125	
Trp	Arg	Val	Lys	Lys	Val	Val	Leu	Met	Ile	Ile	Gln	Val	Ser	Met	Ile	130	135	140	
Phe	Leu	Ile	Leu	Asn	Leu	Leu	Ser	Leu	Ser	Met	Tyr	Asp	Gln	Phe	Ser	145	150	155	160
Ile	Asp	Val	Tyr	Glu	Gly	Asn	Thr	Ser	Tyr	Asn	Leu	Gly	Asp	Ser	Thr	165	170	175	
Pro	Phe	Pro	Thr	Ile	Ser	Leu	Phe	Ile	Asn	Ser	Ser	Lys	Val	Phe	Val	180	185	190	
Ile	Thr	Asn	Ser	Ser	His	Ile	Phe	Leu	Pro	Ile	Asn	Ser	Leu	Phe	Met	195	200	205	
Leu	Ile	Pro	Phe	Thr	Val	Ser	Leu	Val	Ala	Phe	Leu	Met	Leu	Ile	Phe	210	215	220	
Ser	Leu	Trp	Lys	His	His	Lys	Lys	Met	Gln	Val	Asn	Ala	Lys	Pro	Pro	225	230	235	240
Arg	Asp	Ala	Ser	Thr	Met	Ala	His	Ile	Lys	Ala	Leu	Gln	Thr	Gly	Phe	245	250	255	

Ser Phe Leu Leu Leu Tyr Ala Val Tyr Leu Leu Phe Ile Val Ile Gly  
 260 265 270

Met Leu Ser Leu Arg Leu Ile Gly Gly Lys Leu Ile Leu Leu Phe Asp  
 275 280 285

His Ile Ser Gly Ile Gly Phe Pro Ile Ser His Ser Phe Val Leu Ile  
 290 295 300

Leu Gly Asn Asn Lys Leu Arg Gln Ala Ser Leu Ser Val Leu His Cys  
 305 310 315 320

Leu Arg Cys Arg Ser Lys Asp Met Asp Thr Met Gly Pro  
 325 330

<210> 124

<211> 1371

<212> DNA

<213> Mus sp.

<220>

<223> mouse T2R10 (mGR10)

<400> 124

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ctgggattgt ttatatttgt tacaaacaaa tttatatgtt tgtagtcag taatgtataa 180
gtgggatttt aaagcatgat tatcttgaat ttttaacaaa aaacatgtag tgctttttaa 240
atgtagcaga aacattaaaa attgaagcat gttctcacag ataataagca ccagtgatat 300
ttttactttt acaataatat tatttggtga attagtaata ggaatttttag gaaatggatt 360
catagcacta gtgaatatca tggactggac caagagaaga agcatttcat cagcggatca 420
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gaaaatgtgg ggcttcaaag ctggtaggag taatatagag aaggatagga g 1371

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<210> 125

<211> 303

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R11 (mGR11)



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 <222> (169)  
 <223> Xaa = any amino acid  
  
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 20 25 30  
 Leu Met Val Leu Val His Cys Ile Asp Trp Val Lys Arg Lys Lys Phe  
 35 40 45  
 His Leu Leu Ile Lys Ser Ser Pro Leu Trp Gln Thr Ser Arg Ile Cys  
 50 55 60  
 Leu Leu Trp Phe Met Leu Ile His Leu Leu Ile Thr Leu Leu Tyr Ala  
 65 70 75 80  
 Asp Leu Ala Ser Thr Arg Thr Met Met Gln Phe Ala Ser Asn Pro Trp  
 85 90 95  
 Thr Ile Ser Asn His Ile Ser Ile Trp Leu Ala Thr Cys Leu Gly Val  
 100 105 110  
 Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Thr Phe Leu Tyr  
 115 120 125  
 Leu Lys Trp Arg Val Gln Phe Leu Leu Leu Asn Ile Leu Leu Val Lys  
 130 135 140  
 Phe Glu Ile Asn Met Trp Ile Asn Glu Tyr His Gln Ile Asn Ile Pro  
 145 150 155 160  
 Tyr Ser Phe Ile Ser Tyr Tyr Gln Xaa Cys Gln Ile Gln Val Leu Ser  
 165 170 175  
 Leu His Ile Ile Phe Leu Ser Val Pro Phe Ile Leu Ser Leu Ser Thr  
 180 185 190  
 Phe Leu Leu Leu Ile Phe Ser Leu Trp Thr Leu His Gln Arg Met Gln  
 195 200 205  
 Gln His Val Gln Gly Tyr Arg Asp Ala Ser Thr Met Ala His Phe Lys  
 210 215 220  
 Ala Leu Gln Ala Val Ile Ala Phe Leu Leu Ile His Ser Ile Phe Ile  
 225 230 235 240  
 Leu Ser Leu Leu Leu Gln Leu Trp Lys His Glu Leu Arg Lys Lys Pro  
 245 250 255  
 Pro Phe Val Val Phe Cys Gln Val Ala Tyr Ile Ala Phe Pro Ser Ser  
 260 265 270  
 His Ser Tyr Val Phe Ile Leu Gly Asp Arg Lys Leu Arg Gln Ala Cys  
 275 280 285

Leu Ser Val Leu Trp Arg Leu Lys Cys Arg Pro Asn Tyr Val Gly  
 290 295 300

<210> 126  
 <211> 1108  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R11 (mGR11)

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 tagaactaat aaataaaatg gagcatcctt tgaggagaac atttgatttc tcccagagca 180  
 tacttctaac cattttattc attgaattaa taattggact tataagaaat ggattaatgg 240  
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 caccactttg gcaaacttcc agaatttgct tgcctcgtgt catgctaata catctcctga 360  
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 catggactat atctaaccat atcagcatct ggcttgctac atgccttggt gtcttttatt 480  
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 atattccttg attttgactg cataaatt 1108

<210> 127  
 <211> 150  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R12 (mGR12)

<400> 127  
 Gly Ala Ile Val Asn Val Asp Phe Leu Ile Gly Asn Val Gly Asn Gly  
 1 5 10 15  
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 20 25 30  
 Ser Ser Val Asp Gln Leu Leu Thr Ala Leu Ala Val Ser Arg Ile Thr  
 35 40 45  
 Leu Leu Trp Tyr Leu Tyr Ile Met Lys Arg Thr Phe Leu Val Asp Pro  
 50 55 60  
 Asn Ile Gly Ala Ile Met Gln Ser Thr Arg Leu Thr Asn Val Ile Trp  
 65 70 75 80  
 Ile Ile Ser Asn His Phe Ser Ile Trp Leu Ala Thr Thr Leu Ser Ile  
 85 90 95

Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Ile Phe Cys Tyr  
100 105 110

Leu Arg Trp Arg Phe Glu Lys Val Ile Leu Met Ala Leu Leu Val Ser  
115 120 125

Leu Val Leu Leu Phe Ile Asp Ile Leu Val Thr Asn Met Tyr Ile Asn  
130 135 140

Ile Trp Thr Asp Glu Phe  
145 150

<210> 128  
<211> 520  
<212> DNA  
<213> Mus sp.

<220>  
<223> mouse T2R12 (mGR12)

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<210> 129  
<211> 309  
<212> PRT  
<213> Mus sp.

<220>  
<223> mouse T2R13 (mGR13)

<400> 129  
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Phe Ile Met Gly Thr Leu Gly Asn Gly Phe Ile Phe Leu Ile Val Cys  
20 25 30

Ile Asp Trp Val Gln Arg Arg Lys Ile Ser Leu Val Asp Gln Ile Arg  
35 40 45

Thr Ala Leu Ala Ile Ser Arg Ile Ala Leu Ile Trp Leu Ile Phe Leu  
50 55 60

Asp Trp Trp Val Ser Val His Tyr Pro Ala Leu His Glu Thr Gly Lys  
65 70 75 80

Met Leu Ser Thr Tyr Leu Ile Ser Trp Thr Val Ile Asn His Cys Asn  
85 90 95

Phe Trp Leu Thr Ala Asn Leu Ser Ile Leu Tyr Phe Leu Lys Ile Ala  
 100 105 110  
 Asn Phe Ser Asn Ile Ile Phe Leu Tyr Leu Lys Phe Arg Ser Lys Asn  
 115 120 125  
 Val Val Leu Val Thr Leu Leu Val Ser Leu Phe Phe Leu Phe Leu Asn  
 130 135 140  
 Thr Val Ile Ile Lys Ile Phe Ser Asp Val Cys Phe Asp Ser Val Gln  
 145 150 155 160  
 Arg Asn Val Ser Gln Ile Phe Ile Met Tyr Asn His Glu Gln Ile Cys  
 165 170 175  
 Lys Phe Leu Ser Phe Thr Asn Pro Met Phe Thr Phe Ile Pro Phe Val  
 180 185 190  
 Met Ser Thr Val Met Phe Ser Leu Leu Ile Phe Ser Leu Trp Arg His  
 195 200 205  
 Leu Lys Asn Met Gln His Thr Ala Lys Gly Cys Arg Asp Ile Ser Thr  
 210 215 220  
 Thr Val His Ile Arg Ala Leu Gln Thr Ile Ile Val Ser Val Val Leu  
 225 230 235 240  
 Tyr Thr Ile Phe Phe Leu Ser Phe Phe Val Lys Val Trp Ser Phe Val  
 245 250 255  
 Ser Pro Glu Arg Tyr Leu Ile Phe Leu Phe Val Trp Ala Leu Gly Asn  
 260 265 270  
 Ala Val Phe Ser Ala His Pro Phe Val Met Ile Leu Val Asn Arg Arg  
 275 280 285  
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 290 295 300  
 Lys Asn Ile Glu Val  
 305

<210> 130  
 <211> 1199  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R13 (mGR13)

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 ttacactcat attttgaagg aacaatatgt tttaaaggaa tatattaaca aatcttcagc 180  
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 ctgatagtct gcatagactg ggtccaaaga agaaaaatct ctttagtgga tcaaatccgc 360  
 actgctctgg caattagcag aatcgctcta atttggttga tattcctaga ttggtgggtg 420  
 tctgttcatt acccagcatt acatgaaact ggtaagatgt tatcaacata tttgatttcc 480  
 tggacggtga tcaatcattg taacttttgg cttactgcaa acttgagcat cctttatttt 540

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ctcaagatag ccaacttttc taacattatt tttctttatc taaagtttag atctaaaaat 600
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aaaatatatt ctgatgtgtg ttttgatagt gttcaaagaa atgtgtctca aattttcata 720
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gctctgggaa atgctgtttt ttctgtcac ccatttgtca tgattttggg aaacagaaga 1080
ttgagattgg cttctctctc tctgattttt tggctctggg acagggtttaa aaatatagaa 1140
gtataggggc caagaccac caaggaatca ttttccttat cctaaagaaa aatcaggag 1199

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<210> 131  
 <211> 309  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R14 (mGR14)

<400> 131  
 Met Leu Ser Thr Met Glu Gly Val Leu Leu Ser Val Ser Thr Ser Glu  
 1 5 10 15  
 Ala Val Leu Gly Ile Val Gly Asn Thr Phe Ile Ala Leu Val Asn Cys  
 20 25 30  
 Met Asp Tyr Asn Arg Asn Lys Lys Leu Ser Asn Ile Gly Phe Ile Leu  
 35 40 45  
 Thr Gly Leu Ala Ile Ser Arg Ile Cys Leu Val Leu Ile Leu Ile Thr  
 50 55 60  
 Glu Ala Tyr Ile Lys Ile Phe Tyr Pro Gln Leu Leu Ser Pro Val Asn  
 65 70 75 80  
 Ile Ile Glu Leu Ile Ser Tyr Leu Trp Ile Ile Ile Cys Gln Leu Asn  
 85 90 95  
 Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala  
 100 105 110  
 Asn Phe Ser His Tyr Ile Phe Val Trp Leu Lys Arg Arg Ile Asp Leu  
 115 120 125  
 Val Phe Phe Phe Leu Ile Gly Cys Leu Leu Ile Ser Trp Leu Phe Ser  
 130 135 140  
 Phe Pro Val Val Ala Lys Met Val Lys Asp Asn Lys Met Leu Tyr Ile  
 145 150 155 160  
 Asn Thr Ser Trp Gln Ile His Met Lys Lys Ser Glu Leu Ile Ile Asn  
 165 170 175  
 Tyr Val Phe Thr Asn Gly Gly Val Phe Leu Phe Phe Met Ile Met Leu  
 180 185 190  
 Ile Val Cys Phe Leu Leu Ile Ile Ser Leu Trp Arg His Arg Arg Gln  
 195 200 205

Met Glu Ser Asn Lys Leu Gly Phe Arg Asp Leu Asn Thr Glu Val His  
 210 215 220

Val Arg Thr Ile Lys Val Leu Leu Ser Phe Ile Ile Leu Phe Ile Leu  
 225 230 235 240

His Phe Met Gly Ile Thr Ile Asn Val Ile Cys Leu Leu Ile Pro Glu  
 245 250 255

Ser Asn Leu Leu Phe Met Phe Gly Leu Thr Thr Ala Phe Ile Tyr Pro  
 260 265 270

Gly Cys His Ser Leu Ile Leu Ile Leu Ala Asn Ser Arg Leu Lys Gln  
 275 280 285

Cys Ser Val Met Ile Leu Gln Leu Leu Lys Cys Cys Glu Asn Gly Lys  
 290 295 300

Glu Leu Arg Asp Thr  
 305

<210> 132  
 <211> 1535  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R14 (mGR14)

<400> 132

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agtcaaaacta	tggacctcac	aacctgacac	ttcttcagat	gcaaaatatt	ctcacagaga	180
caagtaaaac	atacaaaaca	aatactttta	tttgcctatt	aacaaatggc	aagaaaagat	240
tcaggcttga	acatcctgta	gacaagctaa	ggacaggagc	aactgaaggg	atctccatga	300
agacctttca	gattttctacc	aaaagtaatt	tttaactata	tttaagtctt	ttaaagaaaga	360
aagtaaagcc	actcttttat	tgaacagcaa	tagattggaa	tcttaaacaa	ctgcaacaga	420
agccatttta	aagatcaaca	aagatgctga	gcacaatgga	aggtgtcctc	ctttcagttt	480
caactagtga	ggctgtgctg	ggcattgtag	ggaacacatt	cattgcactt	gtaaactgta	540
tggactataa	caggaacaag	aagctctcta	atattggctt	tattctcact	ggcttggcaa	600
tttccagaat	ttgccttgtg	ttgatcttaa	tcacagaggc	atacataaaa	atattctatc	660
cacagttgct	gtctcctgtc	aacataattg	agctcatcag	ttatctatgg	ataattatct	720
gtcaattgaa	tgtctgggtt	gccactagtc	tcagtatttt	ttatttcctg	aagatagcaa	780
atttttccca	ctacataatt	gtctgggtta	aaagaagaat	tgatttagtt	tttttcttcc	840
tgatagggtg	cttgcttata	tcattggctat	tttctttccc	agttgttgcg	aagatgggta	900
aagataataa	aatgctgtat	ataaacacat	cttggcagat	ccacatgaag	aaaagtgaag	960
taatcattaa	ctatgttttc	accaatgggg	gagtattttt	attttttatg	ataatgttaa	1020
ttgtatgttt	cctgttaatc	atttcacttt	ggagacatcg	caggcagatg	gaatcaaata	1080
aattaggatt	cagagatctc	aacacagaag	ttcatgtgag	aacaataaaa	gtttttattgt	1140
ctttttattat	cctttttata	ttgcatttca	tgggtattac	cataaatgta	atttgtctgt	1200
taatcccaga	aagcaacttg	ttattcatgt	ttggtttgac	aactgcattc	atctatcccg	1260
gctgccactc	acttatccta	attctagcaa	acagtcggct	gaagcagtg	tctgtaaatga	1320
tactgcaact	attaaagtgc	tgtgagaatg	gtaaagaact	cagagacaca	tgacagtctg	1380
gaacacatgc	aatctggaat	tgctcagtga	aaaagtact	gaagatcttt	tcacttgcac	1440
tatgctcttt	tattgatttg	gcattcattat	caaacactgt	tggagccttg	tgaactcttg	1500
ttcagagtct	tctgcctctc	aaggaatcac	actcc			1535

<210> 133  
 <211> 310  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R15 (mGR15)

<400> 133

Met	Cys	Ala	Val	Leu	Arg	Ser	Ile	Leu	Thr	Ile	Ile	Phe	Ile	Leu	Glu
1				5					10					15	
Phe	Phe	Ile	Gly	Asn	Leu	Gly	Asn	Gly	Phe	Ile	Ala	Leu	Val	Gln	Cys
			20					25						30	
Met	Asp	Leu	Arg	Lys	Arg	Arg	Thr	Phe	Pro	Ser	Ala	Asp	His	Phe	Leu
			35				40					45			
Thr	Ala	Leu	Ala	Ile	Ser	Arg	Leu	Ala	Leu	Ile	Trp	Val	Leu	Phe	Leu
	50					55					60				
Asp	Ser	Phe	Leu	Phe	Ile	Gln	Ser	Pro	Leu	Leu	Met	Thr	Arg	Asn	Thr
65					70					75					80
Leu	Arg	Leu	Ile	Gln	Thr	Ala	Trp	Asn	Ile	Ser	Asn	His	Phe	Ser	Ile
				85					90						95
Trp	Phe	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Phe	Lys	Ile	Ala	Ile
			100					105					110		
Phe	Ser	Asn	Tyr	Leu	Phe	Phe	Tyr	Leu	Lys	Arg	Arg	Val	Lys	Arg	Val
		115					120					125			
Val	Leu	Val	Ile	Leu	Leu	Leu	Ser	Met	Ile	Leu	Leu	Phe	Phe	Asn	Ile
	130					135						140			
Phe	Leu	Glu	Ile	Lys	His	Ile	Asp	Val	Trp	Ile	Tyr	Gly	Thr	Lys	Arg
145					150					155					160
Asn	Ile	Thr	Asn	Gly	Leu	Ser	Ser	Asn	Ser	Phe	Ser	Glu	Phe	Ser	Arg
				165					170					175	
Leu	Ile	Leu	Ile	Pro	Ser	Leu	Met	Phe	Thr	Leu	Val	Pro	Phe	Gly	Val
			180						185					190	
Ser	Leu	Ile	Ala	Phe	Leu	Leu	Leu	Ile	Phe	Ser	Leu	Met	Lys	His	Val
		195					200					205			
Arg	Lys	Met	Gln	Tyr	Tyr	Thr	Lys	Gly	Cys	Lys	Asp	Val	Arg	Thr	Met
	210					215					220				
Ala	His	Thr	Thr	Ala	Leu	Gln	Thr	Val	Val	Ala	Phe	Leu	Leu	Leu	Tyr
225					230					235					240
Thr	Thr	Phe	Phe	Leu	Ser	Leu	Val	Val	Glu	Val	Ser	Thr	Leu	Glu	Met
				245					250					255	
Asp	Glu	Ser	Leu	Met	Leu	Leu	Phe	Ala	Lys	Val	Thr	Ile	Met	Ile	Phe
			260					265					270		

Pro Ser Ile His Ser Cys Ile Phe Ile Leu Lys His Asn Lys Leu Arg  
 275 280 285

Gln Asp Leu Leu Ser Val Leu Lys Trp Leu Gln Tyr Trp Cys Lys Arg  
 290 295 300

Glu Lys Thr Leu Asp Ser  
 305 310

<210> 134  
 <211> 1482  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R15 (mGR15)

<400> 134  
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 caagtttacc tgcacagaca agggaagaag tggcaaaatg tgcaaatgag agcaacttta 180  
 tttgactgtc agtacgttga aattcagtgt ttccttaatc agttatggat tgacattttat 240  
 gtgcacagaa cctggaagaa tttcagccaa gctggaggta aaaatccaaa attctgatga 300  
 taaaaccaaaa agtaaatcac aggtaaatct tctttat ttttttttaa tactgtatat 360  
 ggacattttt taatacagca tatttttttt ttgaaattta gaaaaaaacc actaagaaat 420  
 attcaccaat ggaatagact ttaaagtcac ttagagaatg tgtgctgttc tacgtagcat 480  
 actgacaatc attttcattt tggagttcct cattggaaat ctgggggaatg gattcatagc 540  
 tctggtacaa tgcattggact tacgaaagag aagaacgttc ccttcagcag atcatttcct 600  
 cactgctctg gccatctcca ggcttgctct gatatgggtt ttatttctag attcatttct 660  
 gtttatacaa tccccattac tgaatgactag aaatacatta agactgattc agactgcctg 720  
 gaataaagc aatcatttca gtatatgggt tgctaccagc ctcagcatct tttatctctt 780  
 caagatagcc attttttcta actatctttt cttctacctg aagcggagag ttaaaagggt 840  
 ggttttgggt atactgctgc tatccatgat ccttttggtt tttaatatat ttttagaaat 900  
 caaacatatt gatgtctgga tctatggaac caaaagaaac ataactaatg gtttgagttc 960  
 aaacagtttt tcagagtttt ccaggcttat ttttaattcca agtttaaatgt tcacattagt 1020  
 accctttgggt gtatccttga tagctttcct cctcctaatac ttttccctta tgaaacatgt 1080  
 aaggaagatg cagtactaca ccaaaggatg caaagatgtc agaaccatgg cccacaccac 1140  
 agccctgcag actgtgggtg ccttcctcct attatatact actttctttc tgtctctagt 1200  
 tgtggaagtt tcaacacttg aaatggatga aagtctgatg cttctgtttg caaaagttac 1260  
 tataatgatt tttccttcca tccactcctg tattttcatt ttgaaacata ataagttgag 1320  
 acaggacttg ctttcagtac tgaagtggct acagtattgg tgcaagcgtg agaaaacctt 1380  
 ggattcatag accattgtat gcatcacctt gaatattcta gaggggtgta ggttcatatg 1440  
 aaagtattga attttttaaat ttgagccttt tgtatat tttt ct 1482

<210> 135  
 <211> 305  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R16 (mGR16)

<400> 135  
 Met Asn Gly Val Leu Gln Val Thr Phe Ile Val Ile Leu Ser Val Glu  
 1 5 10 15  
 Phe Ile Ile Gly Ile Phe Gly Asn Gly Phe Ile Ala Val Val Asn Ile  
 20 25 30



Lys Asp Leu Val Lys Gly Arg Lys Ile Ser Ser Val Asp Gln Ile Leu  
 35 40 45  
 Thr Ala Leu Ala Ile Ser Arg Ile Ala Leu Leu Trp Leu Ile Leu Val  
 50 55 60  
 Ser Trp Trp Ile Phe Val Leu Tyr Pro Gly Gln Trp Met Thr Asp Arg  
 65 70 75 80  
 Arg Val Ser Ile Met His Ser Ile Trp Thr Thr Phe Asn Gln Ser Ser  
 85 90 95  
 Leu Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala  
 100 105 110  
 Asn Phe Ser Asn Pro Ile Phe Leu Tyr Leu Lys Val Arg Leu Lys Lys  
 115 120 125  
 Val Met Ile Gly Thr Leu Ile Met Ser Leu Ile Leu Phe Cys Leu Asn  
 130 135 140  
 Ile Ile Ile Met Asn Ala Pro Glu Asn Ile Leu Ile Thr Glu Tyr Asn  
 145 150 155 160  
 Val Ser Met Ser Tyr Ser Leu Ile Leu Asn Asn Thr Gln Leu Ser Met  
 165 170 175  
 Leu Phe Pro Phe Ala Asn Thr Met Phe Gly Phe Ile Pro Phe Ala Val  
 180 185 190  
 Ser Leu Val Thr Phe Val Leu Leu Val Phe Ser Leu Trp Lys His Gln  
 195 200 205  
 Arg Lys Met Gln His Ser Ala His Gly Cys Arg Asp Ala Ser Thr Lys  
 210 215 220  
 Ala His Ile Arg Ala Leu Gln Thr Leu Ile Ala Ser Leu Leu Leu Tyr  
 225 230 235 240  
 Ser Ile Phe Phe Leu Ser His Val Met Lys Val Trp Ser Ala Leu Leu  
 245 250 255  
 Leu Glu Arg Thr Leu Leu Leu Leu Ile Thr Gln Val Ala Arg Thr Ala  
 260 265 270  
 Phe Pro Ser Val His Ser Trp Val Leu Ile Leu Gly Asn Ala Lys Met  
 275 280 285  
 Arg Lys Ala Ser Leu Tyr Val Phe Leu Trp Leu Arg Cys Arg His Lys  
 290 295 300  
 Glu  
 305

<210> 136  
 <211> 1316  
 <212> DNA  
 <213> Mus sp.

<220>

<223> mouse T2R16 (mGR16)

<400> 136

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aagcatggtt caaagaatct taagtaatta caatagaaat tgaagcatcc aagtgaagat 180
gaatgggtgtc ctacagggtta catttatagt ctttttgagt gtggaattta taattggcat 240
ctttggcaat ggattcatag cggtggtgaa cataaaggac ttggtcaagg gaaggaagat 300
ctcttcagtg gatcagatcc tcaactgctct ggccatctcc agaattgcac tgctgtggtt 360
aatattagta agttggtgga tatttgtgct ttaccaggga caatggatga ctgatagaag 420
agtttagcata atgcacagta tatggacaac attcaaccag agtagtctct ggtttgctac 480
aagtctcagc atctttttatt ttttcaagat agcaaatttt tccaacccta tttttcttta 540
tttaaagggtc agacttaaaa aagtcatgat agggacattg ataatgtctt tgattctctt 600
ttgttttaaat attatcatta tgaatgcacc tgagaacatt ttaatcactg aatataatgt 660
atctatgtct tacagcttga ttttgaataa cacacagctt tctatgctgt ttccatttgc 720
caacaccatg tttgggttca taccttttgc tgtgtcactg gtcacttttg tccttcttgt 780
tttctccctg tggaaacatc agagaaagat gcaacacagt gcccatggat gcagagatgc 840
cagcactaag gcccacatca gagccttgca gacattgatt gcctccctcc tcctgtattc 900
cattttcttc ctgtctcatg ttatgaaggt ttggagtgtc ctgcttctgg agaggacact 960
cctgcttttg atcacacagg ttgcaagaac agcttttccg tcagtgcact cctgggtcct 1020
gattctgggc aatgctaaga tgagaaaggc ttctctctat gtattcctgt ggctgagggtg 1080
caggcacaaa gaatgaaacc ctacagtgtg cagacctggg gtatatattat gtggatgac 1140
ttacatatct tagaggaaaa tggattaaaa gaaattctca tatttataaa tttttaggtc 1200
tgaattacat aaaaatgtat ataattttt caaagtacaa gatagtagtt tataacttac 1260
atgataaata ctgtctatgc atcttctagt cttttagtaa tatgtaaaaa catgtt 1316
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<210> 137

<211> 330

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R17 (mGR17)

<400> 137

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Met Lys His Phe Trp Lys Ile Leu Ser Val Ile Ser Gln Ser Thr Leu
  1              5              10              15

Ser Val Ile Leu Ile Val Glu Leu Val Ile Gly Ile Ile Gly Asn Gly
      20              25              30

Phe Met Val Leu Val His Cys Met Asp Trp Val Lys Lys Lys Lys Met
      35              40              45

Ser Leu Val Asn Gln Ile Leu Thr Ala Leu Ser Ile Ser Arg Ile Phe
      50              55              60

Gln Leu Cys Leu Leu Phe Ile Ser Leu Val Ile Asn Phe Ser Tyr Thr
      65              70              75              80

Asp Leu Thr Thr Ser Ser Arg Met Ile Gln Val Met Tyr Asn Ala Trp
      85              90              95

Ile Leu Ala Asn His Phe Ser Ile Trp Ile Ala Thr Cys Leu Thr Val
      100             105             110

Leu Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Phe Phe Leu Tyr
      115             120             125
```

Leu Lys Trp Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser  
 130 135 140  
 Leu Leu Leu Leu Ile Leu Asn Ile Leu Leu Thr Asn Leu Glu Thr Asp  
 145 150 155 160  
 Met Trp Thr Asn Glu Tyr Gln Arg Asn Ile Ser Cys Ser Phe Ser Ser  
 165 170 175  
 His Tyr Tyr Ala Lys Cys His Arg Gln Val Leu Arg Leu His Ile Ile  
 180 185 190  
 Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu Leu  
 195 200 205  
 Ile Phe Ser Leu Trp Thr His His Lys Arg Met Gln Gln His Val Gln  
 210 215 220  
 Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln Thr  
 225 230 235 240  
 Val Ile Ala Phe Phe Leu Leu Tyr Ser Ile Phe Ile Leu Ser Val Leu  
 245 250 255  
 Ile Gln Ile Trp Lys Tyr Glu Leu Leu Lys Lys Asn Leu Phe Val Val  
 260 265 270  
 Phe Cys Glu Val Val Tyr Ile Ala Phe Pro Thr Phe His Ser Tyr Ile  
 275 280 285  
 Leu Ile Val Gly Asp Met Lys Leu Arg Gln Ala Cys Leu Pro Leu Cys  
 290 295 300  
 Ile Ile Ala Ala Glu Ile Gln Thr Thr Leu Cys Arg Asn Phe Arg Ser  
 305 310 315 320  
 Leu Lys Tyr Phe Arg Leu Cys Cys Ile Phe  
 325 330

<210> 138  
 <211> 1354  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R17 (mGR17)

<400> 138  
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 agaaaaatac attttatgag aatcaactca gaggttgta gaaattgtcg aaacagcatt 180  
 ttaaaaattt acatctcaac tggatatatg agcaagtctt tataactgat atataaaatg 240  
 aagcactttt ggaagatatt atctgttatc tcccagagca cactttcagt cattttaatc 300  
 gtggaattag taattggaat tataggaaat gggttcatgg tcctgggtcca ctgtatggac 360  
 tgggttaaga aaaagaaaaat gtccctagtt aatcaaattc ttactgcttt gtcaatctcc 420  
 agaatttttc agctctgttt attgtttata agtttagtaa tcaacttttc atatacagat 480  
 ttaactacaa gttcaaggat gatacaagtc atgtacaatg cttggatttt agccaacat 540  
 ttcagcatct ggattgctac atgcctcact gtcccttatt ttctaaagat agccaatttt 600  
 tctaactctt tttttcttta tctaaagtg agagttgaaa aagtagtttc agttacactg 660  
 ttggtgtcat tgctcctcct gattttaaat attttactaa ctaacttgga aaccgacatg 720

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tggacaaatg aatatcaaag aaacatatca tgcagcttca gttctcatta ctatgcaaag 780
tggtcacaggc aggtgttaag gcttcacatt attttctgt ctgtccccgt tgttttgtcc 840
ctgtcaactt ttctcctgct catcttctcc ctgtggacac atcacaagag gatgcagcag 900
catgttcagg gaggcagaga tggcagaacc acggccact tcaaagccct acaaactgtg 960
attgcatttt tcctactata ttccattttt attctgtctg tcttaataca aatttggaaa 1020
tatgaattac tgaagaaaaa tcttttcggt gtattttgtg aggttgtata tatagctttt 1080
ccgacattcc attcatatat tctgattgta ggagacatga agctgagaca ggctgcctg 1140
cctctctgta ttatcgcagc tgaaattcag actacactat gtagaaattt tagatcacta 1200
aagtacttta gattatgttg tatattctag acaaaaatta actgatacaa atgtcttttg 1260
tatttttcat tttaaataatc ctttaatttt gactgcatga aattgatttc tgcttgcaat 1320
tatcactgat taaaactatt aataatttaa ctgag 1354

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<210> 139  
 <211> 299  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R18 (mGR18)

<400> 139

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Met Val Pro Thr Gln Val Thr Ile Phe Ser Ile Ile Met Tyr Val Leu
  1              5              10              15

Glu Ser Leu Val Ile Ile Val Gln Ser Cys Thr Thr Val Ala Val Leu
      20              25              30

Phe Arg Glu Trp Met His Phe Gln Arg Leu Ser Pro Val Glu Thr Ile
      35              40              45

Leu Ile Ser Leu Gly Ile Ser His Phe Cys Leu Gln Trp Thr Ser Met
      50              55              60

Leu Tyr Asn Phe Gly Thr Tyr Ser Arg Pro Val Leu Leu Phe Trp Lys
      65              70              75              80

Val Ser Val Val Trp Glu Phe Met Asn Ile Leu Thr Phe Trp Leu Thr
      85              90              95

Ser Trp Leu Ala Val Leu Tyr Cys Val Lys Val Ser Ser Phe Thr His
      100             105             110

Pro Ile Phe Leu Trp Leu Arg Met Lys Ile Leu Lys Leu Val Leu Trp
      115             120             125

Leu Ile Leu Gly Ala Leu Ile Ala Ser Cys Leu Ser Ile Ile Pro Ser
      130             135             140

Val Val Lys Tyr His Ile Gln Met Glu Leu Val Thr Leu Asp Asn Leu
      145             150             155             160

Pro Lys Asn Asn Ser Leu Ile Leu Arg Leu Gln Gln Phe Glu Trp Tyr
      165             170             175

Phe Ser Asn Pro Leu Lys Met Ile Gly Phe Gly Ile Pro Phe Phe Val
      180             185             190

Phe Leu Ala Ser Ile Ile Leu Leu Thr Val Ser Leu Val Gln His Trp
      195             200             205

```

Val Gln Met Lys His Tyr Ser Ser Ser Asn Ser Ser Leu Lys Ala Gln  
 210 215 220

Phe Thr Val Leu Lys Ser Leu Ala Thr Phe Phe Thr Phe Phe Thr Ser  
 225 230 235 240

Tyr Phe Leu Thr Ile Val Ile Ser Phe Ile Gly Thr Val Phe Asp Lys  
 245 250 255

Lys Ser Trp Phe Trp Val Cys Glu Ala Val Ile Tyr Gly Leu Val Cys  
 260 265 270

Ile His Phe Thr Ser Leu Met Met Ser Asn Pro Ala Leu Lys Lys Ala  
 275 280 285

Leu Lys Leu Gln Phe Trp Ser Pro Glu Pro Ser  
 290 295

<210> 140  
 <211> 2887  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R18 (mGR18)

<220>  
 <221> modified\_base  
 <222> (1083)  
 <223> n = g, a, c or t

<400> 140  
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 aatcaattcc ttaattataa gctattgttt cattatttca tttcctacgt ttttttgc 180  
 ttttactaaa actccaaagc agacattttc taattataat cctacatgta gttagaattt 240  
 taaaaattat atactatttt ctttgcacca ctgagttcag taggttttga aggtttatgc 300  
 ttaacaattg aacattttcat gttagattat tcttgccctc ctaatcttga ataattaaat 360  
 gtccatccag gcttagaatt cacagagtca acagctttca ccttgattct ctactatct 420  
 atcaatgact agaattctgtc tgtcactttt gaaaccgcta attaaatagt tgggtgcttat 480  
 ttaaagggtg ccccatgcc aagagaaaatg tatttcttct ctagatgcct tcgtccttta 540  
 caagttacat gctttactga tgggtgaattg gttttcttcc agttcatctg gggttaagtga 600  
 cctaagaacc tagccatgga aggagaaaca gaagcaaata ttaacgatac aagaacaagt 660  
 tccagaacat tggaaagtac ttagtaaagg cattggaatt agcaaaagaa tagtagcgaa 720  
 gcaaaaaata cttcatctcc attgggaggt caagaaagac tatgcagtgt ttttgatgca 780  
 acttgtcatc tctgagttag acgattcagc acacactttt gagattgaac ttcaacaggt 840  
 ggagccagca gacctgagct ttaggaatga tgggtggaatt tccaagcaaa gacttccgtt 900  
 acctttttga tgtcccctaa caattcgggt gcaatgctca caccgcccaa ctgttgaaat 960  
 gcttgggaaa agggattctg agactggcat tagtatgtca tttgacagaa tggaaacatt 1020  
 gccagggca ttaatgcaca gtaaaggatt caccttttct aagtgtcaa attttaaatt 1080  
 tgnatatttt tagaagacat tatttaaaag aaaggtggag aggatatcca aacagcacct 1140  
 tgagcagata aagaggtgaa gaagaaaaaa caacatgcgt acatgatgga tttctcttta 1200  
 tgaaaatgat caaatgatct taggatcaag aatccacacc tgaatgagat ttgcttgat 1260  
 ccctgtgtga atttgacct acaagcaaa cacagacaaa tgctgtagat agggaaatgt 1320  
 ctatgtcaaa tgtgtgtaag gaggatttgc atccacaaag aagtgcctc ttatactgag 1380  
 agtgctaaga acacattgcc gtttcatatt cggaaagtgg tatagagctg ttgagtcttt 1440  
 ggctaggaag agacttcaga gtggaagcat ggtgccaacg caagtcacca tcttctccat 1500  
 catcatgtat gtgcttgagt ccttagtaat aattgtgcaa agttgcacaa cgggtgcagt 1560  
 gctattcaga gagtggatgc actttcaaag actgtcaccg gtggagacga ttctcatcag 1620  
 cctgggcatc tcacatttct gtctacagtg gacatcaatg ctatacaact ttggtactta 1680

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gacattcttg ttaaccaggt ggcttgctgt cctctactgt gtcaaggtct cttccttcac 1800
tcaccccatc ttcctctggc tgaggatgaa aatcttgaaa ctgggtctct ggttgatact 1860
gggtgctctg atagcttctt gtttgtcaat catcccttct gttgttaa atcacatcca 1920
gatggaatta gtcaccctag ataatttacc caagaacaat tctttgattc taagactaca 1980
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tgctaccttc ttcaccttct tcacatccta ttttctgact atagtcactc cctttattgg 2220
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gagactttgc attggcacag tccctatagt gtaatgcaaa cttgaacaca aacttcaccc 2460
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cccattctct tccgtgccta tccatagtcc ccaggttggt tttgattttt ctcatgatca 2580
caccaactct gcttagcttt tgccaccact gtaatagtaa acatggggtg ttctatatat 2640
tacagtcaaa atcattctca cattgttgat tgcctcacia attcatataa atcccccttc 2700
ctgtcaggaa tttattgtct gctcacttaa tgctcaccat atattaaagc cattaattcc 2760
cccttcctac cttgagttta agaaggaaaa tgtcttacca ttgccacaaa cctattctgc 2820
tgcttctaga cttttatgca agtgatttat acacacacac acacacacac acacacatac 2880
aaacaac

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<210> 141  
 <211> 335  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R19 (mGR19)

<400> 141  
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 1 5 10 15  
 Phe Leu Thr Gly Val Leu Ala Asn Gly Leu Ile Val Val Val Asn Ala  
 20 25 30  
 Ile Asp Leu Ile Met Trp Lys Lys Met Ala Pro Leu Asp Leu Leu Leu  
 35 40 45  
 Phe Cys Leu Ala Thr Ser Arg Ile Ile Leu Gln Leu Cys Ile Leu Phe  
 50 55 60  
 Ala Gln Leu Gly Leu Ser Cys Leu Val Arg His Thr Leu Phe Ala Asp  
 65 70 75 80  
 Asn Val Thr Phe Val Tyr Ile Ile Asn Glu Leu Ser Leu Trp Phe Ala  
 85 90 95  
 Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Ile Ala Thr Ile Pro His  
 100 105 110  
 Pro Leu Phe Leu Trp Leu Lys Met Arg Ile Ser Arg Leu Val Pro Trp  
 115 120 125  
 Leu Ile Leu Ala Ser Val Val Tyr Val Thr Val Thr Thr Phe Ile His  
 130 135 140  
 Ser Arg Glu Thr Ser Glu Leu Pro Lys Gln Ile Phe Ile Ser Phe Phe  
 145 150 155 160

Ser Lys Asn Thr Thr Arg Val Arg Pro Ala His Ala Thr Leu Leu Ser  
 165 170 175  
 Val Phe Val Phe Gly Leu Thr Leu Pro Phe Leu Ile Phe Thr Val Ala  
 180 185 190  
 Val Leu Leu Leu Leu Ser Ser Leu Trp Asn His Ser Arg Gln Met Arg  
 195 200 205  
 Thr Met Val Gly Thr Arg Glu Pro Ser Arg His Ala Leu Val Ser Ala  
 210 215 220  
 Met Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Leu Ser His Asp Met  
 225 230 235 240  
 Val Ala Val Leu Ile Cys Thr Gln Gly Leu His Phe Gly Ser Arg Thr  
 245 250 255  
 Phe Ala Phe Cys Leu Leu Val Ile Gly Met Tyr Pro Ser Leu His Ser  
 260 265 270  
 Ile Val Leu Ile Leu Gly Asn Pro Lys Leu Lys Arg Asn Ala Lys Thr  
 275 280 285  
 Phe Ile Val His Cys Lys Cys Cys His Cys Ala Arg Ala Trp Val Thr  
 290 295 300  
 Ser Arg Asn Pro Arg Leu Ser Asp Leu Pro Val Pro Ala Thr His His  
 305 310 315 320  
 Ser Ala Asn Lys Thr Ser Cys Ser Glu Ala Cys Ile Met Pro Ser  
 325 330 335

<210> 142  
 <211> 1698  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R19 (mGR19)

<400> 142  
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 ttgtatgatg ctccaggatg cctcattagc attgaggaca atcataatta agtaaggcaa 180  
 ggcatgaagg tggctctcac taggtacctg gaggtctctg gttgcatgat ttacttggtga 240  
 tgactctgac acttaagaag acctgaaaaa tgcaaaagct gtcataaggc acagttcgtt 300  
 tctatgggtat ctcttcctta tttgactgac attgagttga gaaggcagca ctataaacia 360  
 atgggccccca ccttcctctt ccattgtctt tgggttggca tcatctccaa aggaaccttg 420  
 gtctagttga aagaagccag aaatcataca tggctgagac tgtgcataac tctatgtatc 480  
 atttaaagaa gtcattgggtt cttcttattt taaaatgatg gaaggtcata tgctcttctt 540  
 ccttctggtc gtggtagtgc agtttttaac tggggtcttg gcaaatggcc tcattgtggt 600  
 tgtcaatgcc atcgacttga tcatgtggaa gaaaatggcc ccaactggatc tgcttctttt 660  
 ttgcctggcg acttctcgga tcattcttca atttgtgtata ttgtttgcac agctgggtct 720  
 atcctgtttg gtgagacaca cgttatttgc tgacaatgtt acctttgtct acattataaa 780  
 cgaactgagt ctctgggttg ccacatggct tgggtgtttc tactgtgcca agattgctac 840  
 catccctcac ccactcttct tgtggctgaa gatgaggata tccaggttg tgccatggct 900  
 gatcctggca tctgtggtct atgtaactgt tactactttc atccatagca gagagacttc 960  
 agaacttcct aagcaaactt ttataagctt tttttctaaa aatacaactc gggtcagacc 1020  
 agcgcagtgc acactactct cagtctttgt ctttgggctc acactaccat ttctcatctt 1080

cactgttgct gttctgctct tgttgctct cctgtggaac cacagccggc agatgaggac 1140  
 tatgggtgga actagggaaac ctagcagaca tgccctcgtc agtgcgatgc tctccattct 1200  
 gtcattcctc atcctctatc tctcccatga catggtagct gttctgatct gtaccaagg 1260  
 cctccacttt ggaagcagaa cctttgcatt ctgcttattg gttattggta tgtaccctc 1320  
 cttacactcg attgtcttaa ttttaggaaa ccctaagctg aaacgaaatg caaaaacgtt 1380  
 cattgtccat tgtaagtgtt gtcattgtgc aagagcttgg gtcacctcaa ggaacccaag 1440  
 actcagcgac ttgccagtgc ctgctactca tcaactcagcc aacaagacat cctgctcaga 1500  
 agcctgtata atgccatctt aattgtccaa cctgaggctt aatcatttca aagggtaaat 1560  
 tgatgatcaa agcccaacac atgatatgac atcaagggtc atatcccagt agtcatgtgg 1620  
 aaataccacc ttgcaaaatg atgtcattga gaaaccaggg caaatggagt ctaggtcttt 1680  
 cagtatgatt tgctgcag 1698

<210> 143  
 <211> 295  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R20 (mGR20)

<400> 143  
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 Leu Leu Gly Asn Cys Ala Asn Val Phe Ile Thr Ile Val Asn Phe Ile  
 20 25 30  
 Asp Cys Val Lys Arg Arg Lys Ile Ser Ser Ala Asp Arg Ile Ile Thr  
 35 40 45  
 Ala Ile Ala Ile Phe Arg Ile Gly Leu Leu Trp Ala Met Leu Thr Asn  
 50 55 60  
 Trp His Ser His Val Phe Thr Pro Asp Thr Asp Asn Leu Gln Met Arg  
 65 70 75 80  
 Val Phe Gly Gly Ile Thr Trp Ala Ile Thr Asn His Phe Thr Thr Trp  
 85 90 95  
 Leu Gly Thr Ile Leu Ser Met Phe Tyr Leu Phe Lys Ile Ala Asn Phe  
 100 105 110  
 Ser Asn Ser Leu Phe Leu His Leu Lys Arg Lys Leu Asp Asn Val Leu  
 115 120 125  
 Leu Val Ile Phe Leu Gly Ser Ser Leu Phe Leu Val Ala Tyr Leu Gly  
 130 135 140  
 Met Val Asn Ile Lys Lys Ile Ala Trp Met Ser Ile His Glu Gly Asn  
 145 150 155 160  
 Val Thr Thr Lys Ser Lys Leu Lys His Val Thr Ser Ile Thr Asn Met  
 165 170 175  
 Leu Leu Phe Ser Leu Ile Asn Ile Val Pro Phe Gly Ile Ser Leu Asn  
 180 185 190  
 Cys Val Leu Leu Leu Ile Tyr Ser Leu Ser Lys His Leu Lys Asn Met  
 195 200 205



Lys Phe Tyr Gly Lys Gly Cys Gln Asp Gln Ser Thr Met Val His Ile  
 210 215 220  
 Lys Ala Leu Gln Thr Val Val Ser Phe Leu Leu Leu Tyr Ala Thr Tyr  
 225 230 235 240  
 Ser Ser Cys Val Ile Ile Ser Gly Trp Ser Leu Gln Asn Ala Pro Val  
 245 250 255  
 Phe Leu Phe Cys Val Thr Ile Gly Ser Phe Tyr Pro Ala Gly His Ser  
 260 265 270  
 Cys Ile Leu Ile Trp Gly Asn Gln Lys Leu Lys Gln Val Phe Leu Leu  
 275 280 285  
 Leu Leu Arg Gln Met Arg Cys  
 290 295

<210> 144  
 <211> 1394  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R20 (mGR20)

<400> 144  
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 atttgaagca atggaccaga attcctcttt atttgactct tagcaaattg gaatgcagca 180  
 tcctttcaag agcagcactg aaatatacca gtcaatggca gagagtaaaa aagtatgcaa 240  
 ttggagacat tatggtaata taaattttcca ttaaaaatga gactgcattc acctattaca 300  
 acacattgct attctgctca acacagagtt aaaaagaaac aagaactctt gtatacattc 360  
 agttagtcac aagtataatt atgttcacat attttaaaaa aatgaatcat gatctgtgaa 420  
 ttgagcctgg ctttttttgt ctctctcttt ttattctttt ccttttagaca gacacaatga 480  
 atttggtaga atggattgtt accatcataa tgatgacaga atttctctta ggaaactgtg 540  
 ccaatgtctt cataaccata gtgaacttca tgcactgtgt gaagagaaga aagatctcct 600  
 cagctgatcg aattataact gctattgcca tcttcagaat tgggtttgtg tgggcaatgt 660  
 taacgaactg gcattcacat gtgtttactc cagacacaga caatttaca atgagagttt 720  
 tcggtggaat tacctgggct ataaccaacc attttaccac ttggctgggg accatactga 780  
 gcatgtttta tttattcaag atagccaatt tttccaacag tctatttctt catctaaaaa 840  
 gaaaacttga caatgttcta cttgtgattt tcctgggac gtctctgttt ttggttgcac 900  
 atcttgggat ggtgaacatc aagaagattg cttggatgag tattcatgaa ggaaatgtga 960  
 ccacaaagag caaactgaag catgtaacaa gcatcacaaa tatgcttctc ttcagcctga 1020  
 taaacattgt accatttggt atatcaactga actgtgttct gctcttaatc tattccctga 1080  
 gtaaaccatct caagaatatg aaattctatg gcaaaggatg tcaagatcag agcaccatgg 1140  
 tccacataaa ggccttgcaa actgtggtct cttttctctt gttatatgcc acatactctt 1200  
 cctgtgtcat tatatcaggt tggagtttgc aaaatgcacc agtcttcctg ttttgtgtga 1260  
 caattggatc cttctaccca gcaggtcatt cttgtatctt gatttgggga aaccagaaac 1320  
 ttaaacaggt ctttctgttg ttgctgagggc agatgagatg ctgactgaaa aaatgaaagt 1380  
 ccccctgtct ctgac 1394

<210> 145  
 <211> 305  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R21 (mGR21)

<400> 145  
Met Gly Ser Asn Val Tyr Gly Ile Leu Thr Met Val Met Ile Ala Glu  
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20 25 30  
Ile Asp Trp Val Arg Lys Gly Thr Leu Ser Ser Ile Gly Trp Ile Leu  
35 40 45  
Leu Phe Leu Ala Ile Ser Arg Met Val Leu Ile Trp Glu Met Leu Ile  
50 55 60  
Thr Trp Ile Lys Tyr Met Lys Tyr Ser Phe Ser Phe Val Thr Gly Thr  
65 70 75 80  
Glu Leu Arg Gly Ile Met Phe Thr Trp Val Ile Ser Asn His Phe Ser  
85 90 95  
Leu Trp Leu Ala Thr Ile Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala  
100 105 110  
Ser Phe Ser Lys Pro Val Phe Leu Tyr Leu Lys Trp Arg Glu Lys Lys  
115 120 125  
Val Leu Leu Ile Val Leu Leu Gly Asn Leu Ile Phe Leu Met Leu Asn  
130 135 140  
Ile Leu Gln Ile Asn Lys His Ile Glu His Trp Met Tyr Gln Tyr Glu  
145 150 155 160  
Arg Asn Ile Thr Trp Ser Ser Arg Val Ser Asp Phe Ala Gly Phe Ser  
165 170 175  
Asn Leu Val Leu Leu Glu Met Ile Val Phe Ser Val Thr Pro Phe Thr  
180 185 190  
Val Ala Leu Val Ser Phe Ile Leu Leu Ile Phe Ser Leu Trp Lys His  
195 200 205  
Leu Gln Lys Met His Leu Asn Ser Arg Gly Glu Arg Asp Pro Ser Thr  
210 215 220  
Lys Ala His Val Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu  
225 230 235 240  
Tyr Ala Thr Tyr Phe Ile Ser Phe Phe Leu Ser Leu Ile Pro Met Ala  
245 250 255  
His Lys Thr Arg Leu Gly Leu Met Phe Ser Ile Thr Val Gly Leu Phe  
260 265 270  
Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly His Ser Asn Leu  
275 280 285  
Arg Gln Ala Ser Leu Trp Val Met Thr Tyr Leu Lys Cys Gly Gln Lys  
290 295 300  
His  
305

<210> 146  
 <211> 2567  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R21 (mGR21)

<400> 146  
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 ccattcccag gcatccaagg atccctgtgt attaaaaggc aacaaagcag aaccaaattgt 180  
 tctgttttg acatgagctt cttccaattc aactgctgaa aaatttggat aactacatat 240  
 aaaactaaga acacagagtg tcacagagca gtctctgctc tccaattcac caggattaat 300  
 attgacagac ccaaaaagatg tcatttaggt aaatttggga tgaatcatat tgttgtcacc 360  
 tttgtgctct agaacataag ctgatagaat caaattttct ttagcagaga caatgcaa 420  
 tgatataaca gtgaaagaga atatatcttt atttgcattg tagcaaata cagctggatg 480  
 cacttcatga ttttctgcaa tctagtccag tctttagaag gatatatata tatatatata 540  
 tatatatata tatatatata tatatatata tataaacctt agtcttgaaa gatatcagaa 600  
 agaaggattt cacaagaatg tacagagcca ttagcaaaat tttaatatat tcatcgacat 660  
 taggtcagtc actacataag aaggacttga atgaaagctt atcttagttt ttgagactac 720  
 agggacattt caccttgcca aatgagaagc agtgagctct ctttgtctgg acatgggaag 780  
 caatgtgtat ggtatcttaa ctatggttat gattgcagag tttgtatttg gaaatatgag 840  
 caatggattc atagtgtga taaactgcat tgattgggtc aggaaaggaa ctctttcttc 900  
 cattgggttg atcctgcttt tcttgccat ttcaagaatg gtgttgatat gggaaatgtt 960  
 aataacatgg ataaaatata tgaagtattc attttcattt gtgactggaa cagaattacg 1020  
 gggatatcatg tttacctggg taatttccaa tcacttcagt ctctggcttg ccactattct 1080  
 cagcatcttt tatttgctca aaatagccag tttctccaaa ccgggttttc tctatttgaa 1140  
 gtggagagag aagaaagtgc ttctgattgt ccttctggga aatttgatct tcttgatgct 1200  
 caacatatta caaataaaca aacatataga acactggatg tatcaatatg agagaaatag 1260  
 aacttggagt tctagagtga gtgactttgc aggggtttca aatctggctt tattggagat 1320  
 gattgtgttc tctgtaacac cattcacagt ggccctggtc tcttcatcc tgttaattct 1380  
 ctcttgttg aaacatctac agaaaatgca tctcaattct agaggggaac gagacccag 1440  
 cactaaagcc catgtgaatg ccttgagaat tatggctctc tctctctac tctatgccac 1500  
 ttacttcata tctttttttc tatcattgat tcccatggca cataaaacac gactgggtct 1560  
 tatgtttagc ataactgttg ggcttttcta cccttcaagc cactcattta tcttaatttt 1620  
 gggacattct aatttaaggc aagccagtct ttgggtgatg acatatctta aatgtgggca 1680  
 aaagcattag aatttcacta ttccataagg cagccaaacc acgtgctact aggtatatga 1740  
 tactactcag tggtaaagcc ctaggcaaac attaacctta gaaaatatat aattttgtga 1800  
 ctcttctgta tttgataaat cactcacata tttagaagaa tgctacagta gtgtgatctt 1860  
 gtacatgatt gtaacaattc aattttatta atatagttca ggcattgata cataccctg 1920  
 ataactgaaa agtaagttag atgctacata tatatttaga tctagactta ggggcaaaga 1980  
 gagaccagc tgatagctgt gcaataaaga ttttaatttt catcctgttg tgagtattct 2040  
 gaaatctatg tctactgaag cataagcaag attttcacac actgaaacaa tctcttatgc 2100  
 tttcttatat tgttttaaaa gtaaattaga aaatttaaat aaacttaatg gcaattgaaa 2160  
 ttacaaaagc taaacacatg tggttattag aaattagact gtatgtaggt ctaggggat 2220  
 ggcttagtaa agtgctttgt tgcaagcttc aggatattat tctaaatccc tagattcaat 2280  
 taaaaacctg gcataaatag ccaatgtaaa atttgtctgt aaaatgtaac cagtgttaag 2340  
 agtaccaga caacaaatg tttactttta aaaccattta ttgatattct tttaaaaata 2400  
 ggtatgtatt ttactattta aataagattt tgtcaaaagc tagtcttgac acctaggta 2460  
 aacataggaa ggcaacaagt ttgaagtcag ctactgggga cagtgtctgct agcagctgac 2520  
 agaggccact gctgactaca gcagatcatt tacaggttca gcactag 2567

<210> 147  
 <211> 309  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R22 (mGR22)

<400> 147

Met Ser Ser Leu Leu Glu Ile Phe Phe Val Ile Ile Ser Val Val Glu  
1 5 10 15  
Phe Ile Ile Gly Thr Leu Gly Asn Gly Phe Ile Val Leu Ile Asn Ser  
20 25 30  
Thr Ser Trp Phe Lys Asn Gln Lys Ile Ser Val Ile Asp Phe Ile Leu  
35 40 45  
Thr Trp Leu Ala Ile Ser Arg Met Cys Val Leu Trp Thr Thr Ile Ala  
50 55 60  
Gly Ala Ser Leu Arg Lys Phe Tyr Lys Thr Leu Ser Tyr Ser Lys Asn  
65 70 75 80  
Phe Lys Phe Cys Phe Asp Ile Ile Trp Thr Gly Ser Asn Tyr Leu Cys  
85 90 95  
Ile Ala Cys Thr Thr Cys Ile Ser Val Phe Tyr Leu Phe Lys Ile Ala  
100 105 110  
Asn Phe Ser Asn Ser Ile Phe Phe Trp Ile Lys Gln Arg Ile His Ala  
115 120 125  
Val Leu Leu Ala Ile Val Leu Gly Thr Leu Met Tyr Phe Ile Leu Phe  
130 135 140  
Leu Ile Phe Met Lys Met Ile Ala Asn Asn Phe Ile Tyr Lys Trp Thr  
145 150 155 160  
Lys Leu Glu Gln Asn Thr Thr Phe Pro Val Leu Asp Thr Leu Ser Gly  
165 170 175  
Phe Leu Val Tyr His Ser Leu Tyr Asn Gly Ile Leu Ile Phe Phe Phe  
180 185 190  
Ile Val Ser Leu Thr Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Ser  
195 200 205  
His Leu Arg Arg Met Lys Leu Gln Gly Ile His Thr Lys Asp Ile Ser  
210 215 220  
Thr Glu Ala His Ile Lys Ala Met Lys Thr Met Met Ser Phe Leu Leu  
225 230 235 240  
Phe Phe Ile Ile Tyr Tyr Ile Ser Asn Ile Met Leu Ile Val Ala Ser  
245 250 255  
Ser Ile Leu Asp Asn Val Val Ala Gln Ile Phe Ser Tyr Asn Leu Ile  
260 265 270  
Phe Leu Tyr Leu Ser Val His Pro Phe Leu Leu Val Leu Trp Asn Ser  
275 280 285  
Lys Leu Lys Trp Thr Phe Gln His Val Leu Arg Lys Leu Val Cys His  
290 295 300  
Cys Gly Gly Tyr Ser  
305

<210> 148  
 <211> 1488  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R22 (mGR22)

<400> 148  
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 aatacatatt caaataccag cacaatgttt caaatttaaa atataaacat tataaaaccc 120  
 agcagagAAC aaaatgatag ccttgataat tgttggtttg ctcaagaaaa atgggtgtat 180  
 actttaacat ttaattggga actcagttga gagcatatat ttaggggttt acagagggtat 240  
 tcattgcccc ttttaagattt ggattcacac atctacatca atgtggctgt aatccatttt 300  
 cccatgatga aataaggtag agactgccta ttaaagcaca tgtcgagcct actggagatt 360  
 ttctttgtga tcatttcggt tgtagaattc ataataaggaa ctttgggaaa tggattttatt 420  
 gtcctgataa acagtacttc ttggttcaag aatcagaaaa tctctgtaat tgatttcatt 480  
 cttacttggg tggccatctc cagaatgtgt gttctatgga caacaattgc tgggtgcctct 540  
 ctcaggaaat tctacaagac gttaagttac tctaagaatt tcaaattttg ttttgacatt 600  
 atctggacag gatccaacta tttatgcata gcctgtacaa cgtgcatcag tgtcttctac 660  
 ttgttcaaga ttgccaactt ttctaattcc attttcttct ggattaaaca gagaattcat 720  
 gcagtacttc tggctattgt cctaggcaca ctcatgtatt tcattttatt tctcattttt 780  
 atgaaaatga tagctaataa ttttatctac aaatggacaa aattggaaca aaacacaaca 840  
 ttccctgttt tagatactct aagtggtttc ttagtctacc atagcctcta caatgggatt 900  
 ctcattttct tttttatagt gtctctgacc tcatttcttc ttttaattct ctctttatgg 960  
 agccacctta ggaggatgaa actacagggc atacatacca aagacataag cacagaagca 1020  
 cacataaaag ctatgaaaac tatgatgtca ttcttttgt tcttcatcat atattatatt 1080  
 agcaacatta tgcttattgt ggcaagctcc attcttgaca atgtggttgc acaaattttc 1140  
 tcttataacc taatatttct gtattttatct gttcatcctt ttcttctggt tttatggaac 1200  
 agcaaatgaa aatggacatt ccagcatgta ttgagaaagc tgggtgtgtca ttgtggaggt 1260  
 tattcttgat ttcagtaaat acactcaata taactgatgg atttctaagg taagaaaaat 1320  
 ggaacaagga ataaagagga gaaatatatt ccttttcaga tcatctgctc tgtcattctg 1380  
 tccttagcat gctattaaga attgttgact aaatccagtc atttttaaca tgaggaaagg 1440  
 atgtttcaat ccaacttaga gaggggtacaa aatagtccta ggaggcag 1488

<210> 149  
 <211> 333  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R23 (mGR23)

<400> 149  
 Met Phe Ser Gln Lys Ile Asn Tyr Ser His Leu Phe Thr Phe Ser Ile  
 1 5 10 15  
 Thr Leu Tyr Val Glu Ile Val Thr Gly Ile Leu Gly His Gly Phe Ile  
 20 25 30  
 Ala Leu Val Asn Ile Met Asp Trp Val Lys Arg Arg Arg Ile Ser Ser  
 35 40 45  
 Val Asp Gln Ile Leu Thr Ala Leu Ala Leu Thr Arg Phe Ile Tyr Val  
 50 55 60  
 Leu Ser Met Leu Ile Cys Ile Leu Leu Phe Met Leu Cys Pro His Leu  
 65 70 75 80

Pro Arg Arg Ser Glu Met Leu Ser Ala Met Gly Ile Phe Trp Val Val  
                     85                    90                    95  
 Asn Ser His Phe Ser Ile Trp Leu Thr Thr Cys Leu Gly Val Phe Tyr  
                     100                    105                    110  
 Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Phe Phe Leu Tyr Leu Lys  
                     115                    120                    125  
 Trp Arg Val Lys Lys Val Ile Leu Ile Ile Ile Leu Ala Ser Leu Ile  
                     130                    135                    140  
 Phe Leu Thr Leu His Ile Leu Ser Leu Gly Ile Tyr Asp Gln Phe Ser  
 145                    150                    155                    160  
 Ile Ala Ala Tyr Val Gly Asn Met Ser Tyr Ser Leu Thr Asp Leu Thr  
                     165                    170                    175  
 Gln Phe Ser Ser Thr Phe Leu Phe Ser Asn Ser Ser Asn Val Phe Leu  
                     180                    185                    190  
 Ile Thr Asn Ser Ser His Val Phe Leu Pro Ile Asn Ser Leu Phe Met  
                     195                    200                    205  
 Leu Ile Pro Phe Thr Val Ser Leu Val Ala Phe Leu Met Leu Ile Phe  
                     210                    215                    220  
 Ser Leu Trp Lys His His Lys Lys Met Gln Val Asn Ala Lys Gln Pro  
 225                    230                    235                    240  
 Arg Asp Val Ser Thr Met Ala His Ile Lys Ala Leu Gln Thr Val Phe  
                     245                    250                    255  
 Ser Phe Leu Leu Leu Tyr Ala Ile Tyr Leu Leu Phe Leu Ile Ile Gly  
                     260                    265                    270  
 Ile Leu Asn Leu Gly Leu Met Glu Lys Ile Val Ile Leu Ile Phe Asp  
                     275                    280                    285  
 His Ile Ser Gly Ala Val Phe Pro Ile Ser His Ser Phe Val Leu Ile  
                     290                    295                    300  
 Leu Gly Asn Ser Lys Leu Arg Gln Ala Ser Leu Ser Val Leu Pro Cys  
 305                    310                    315                    320  
 Leu Arg Cys Gln Ser Lys Asp Met Asp Thr Met Gly Leu  
                     325                    330

<210> 150  
 <211> 1442  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R23 (mGR23)

<400> 150  
 aattttcagc aaccaatatg tagactgctt aaatgcatca gaaacattat aaattgaagc 60  
 atgttttcac agaaaataaa ctacagccat ttgtttactt tttcaatcac cttgtatgtg 120  
 gaaatagtaa cggaatctt aggacatgga ttcatagcat tagtgaacat catggactgg 180

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gtcaaaagaa gaaggatctc ttcagtggat cagattctca ctgctttggc ccttaccaga 240
ttcattttatg tcttgtctat gctgatttgc atattgttat tcatgctgtg cccacatttg 300
cctaggagat cagaaatgct ttcagcaatg ggtattttct gggtagtcaa cagccatttt 360
agcatctggc ttactacatg cctcgggtgc ttttattttc tcaagatagc caatttttct 420
aactcttttt ttctttatct aaagtggaga gttaaaaaag tgattttaat aataatcctg 480
gcatcactga ttttcttgac tttacacatt ttatctttag ggatatatga tcagttctca 540
attgctgctt atgtaggaaa tatgtcttat agtttgacag atttaacaca attttccagt 600
actttcttat tctccaactc atccaatggt ttcttaatca ccaactcacc ccatgttttc 660
ttacccatca actccctggt catgctcata cccttcacag tgtccctggg agcctttctc 720
atgctcatct tctcactgtg gaagcatcac aaaaagatgc aggtcaatgc caaacaacct 780
agagatgtca gtactatggc ccacattaaa gccttgcaaa ctgtgttctc cttcctgctg 840
ctgtatgcca tatacttact tttccttacc ataggaattt tgaaccttgg attgatggag 900
aaaatagtga tactgatatt tgaccacatt tctggagcag tttttcctat aagccactca 960
tttgtactga ttctgggaaa cagtaagctg agacaagcca gtctttctgt gttgccttgt 1020
ctaagggtgcc agtccaaaga tatggacacc atgggtctct agtaaatcc agagtacatt 1080
ttgtaaaaat cttgaggatg atcagttcat agaaaaaagt taccttatgg gggaaaaataa 1140
aaagtggggc ttcaatcctg ggagtaataa tacacaggag ggtaggacag catgaaggag 1200
actagcacta tataagtggg ctcatacagg atatgggaaa ggaaagattt atgcaataaa 1260
gagggagatc atattggagg atgaggaggc attacatatg taaaatgact ataagaatgg 1320
aatcatgcta atctaaaaaa atctgtaatg catttcattc agactatata catatatgcc 1380
tatatatgga tatatgggga tatatattct atacatattt taaaagaacc tttcttatat 1440
ag

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<210> 151  
 <211> 309  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R24 (mGR24)

<400> 151  
 Met Val Pro Val Leu His Ser Leu Ser Thr Ile Ile Leu Ile Ala Glu  
 1 5 10 15  
 Phe Val Trp Gly Asn Leu Ser Asn Gly Leu Ile Val Leu Lys Asn Cys  
 20 25 30  
 Ile Asp Trp Ile Asn Lys Lys Glu Leu Ser Thr Val Asp Gln Ile Leu  
 35 40 45  
 Ile Val Leu Ala Ile Ser Arg Ile Ser Leu Ile Trp Glu Thr Leu Ile  
 50 55 60  
 Ile Trp Val Lys Asp Gln Leu Ile Ser Ser Ile Thr Ile Glu Glu Leu  
 65 70 75 80  
 Lys Ile Ile Val Phe Ser Phe Ile Leu Ser Ser His Phe Ser Leu Trp  
 85 90 95  
 Leu Ala Thr Ala Leu Ser Ile Phe Tyr Leu Phe Arg Ile Pro Asn Cys  
 100 105 110  
 Tyr Trp Gln Ile Phe Leu Tyr Leu Lys Trp Arg Ile Lys Gln Leu Ile  
 115 120 125  
 Val His Met Leu Leu Gly Ser Leu Val Phe Leu Val Ala Asn Met Ile  
 130 135 140

Gln Ile Thr Ile Thr Leu Glu Glu Arg Phe Tyr Gln Tyr Gly Gly Asn  
 145 150 155 160  
 Thr Ser Val Asn Ser Met Glu Thr Glu Phe Ser Ile Leu Ile Glu Leu  
 165 170 175  
 Met Leu Phe Asn Met Thr Met Phe Ser Ile Ile Pro Phe Ser Leu Ala  
 180 185 190  
 Leu Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln  
 195 200 205  
 Lys Met Pro Leu Asn Ser Arg Gly Asp Arg Asp Pro Ser Ala Thr Ala  
 210 215 220  
 His Arg Asn Ala Leu Arg Ile Leu Val Ser Phe Leu Leu Leu Tyr Thr  
 225 230 235 240  
 Ile Tyr Phe Leu Ser Leu Leu Ile Ser Trp Val Ala Gln Lys Asn Gln  
 245 250 255  
 Ser Glu Leu Val His Ile Ile Cys Met Ile Thr Ser Leu Val Tyr Pro  
 260 265 270  
 Ser Phe His Ser Tyr Ile Leu Ile Leu Gly Asn Tyr Lys Leu Lys Gln  
 275 280 285  
 Thr Ser Leu Trp Val Met Arg Gln Leu Gly Cys Arg Met Lys Arg Gln  
 290 295 300  
 Asn Thr Pro Thr Thr  
 305

<210> 152  
 <211> 1465  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R24 (mGR24)

<400> 152  
 caaagaggag aaatatttag ctacacagtg taccacatac aagccgttca atcagtataa 60  
 ggggagcagt catatagaat ttgggctttc tttcttttaa tatggtacct gttctgcaca 120  
 gtctctccac catcatacta attgcagagt ttgtttgggg aaatttgagc aatggtttga 180  
 tagtgttgaa gaactgcatt gactggatca ataaaaaaga gctctccaca gttgatcaaa 240  
 tactcattgt cttggcaatt tcaagaatta gtctcatctg ggaaacacta attatatggg 300  
 ttaaagatca actaatttca tctattacta ttgaagaatt aaaaataatt gtgttcagct 360  
 ttatactatc tagccacttc agtctctggc ttgctacagc tctcagcatc ttctatttat 420  
 tcagaatacc taattgctac tggcagatct ttctctactt gaaatggaga ataaagcaac 480  
 tgattgtcca catgcttctg ggaagcttgg tgttcttggt tgcaaataatg atacagataa 540  
 ccatcactct tgaagagagg ttctatcaat atggaggaaa tacaagtgtg aattccatgg 600  
 agactgagtt ctcaattttg atagagctga tggtatttaa catgactatg ttctccatta 660  
 taccattttc attggcctta atttcttttc ttctgctaatt cttctcttta tggaaacatc 720  
 tcagaagat gccactcaat tctagaggag atagagaccc tagtgctacg gccacagaa 780  
 atgccttgag aattttgggc tccttctctt tgctctatac tatatatttc ctgtctcttc 840  
 ttatatcatg ggttgctcag aagaatcaaa gtgaactggg tcacattatt tgtatgataa 900  
 cttcactcgt gtatccttca ttccactcat atatcctgat tctgggaaat tataaattaa 960  
 agcagacctc tctttgggta atgaggcagc tgggatgtag gatgaaaaga cagaatacac 1020  
 caactacata aggcagccaa acagtctatt ggggttttaga taacaaatct aaatctatga 1080



ggaagtagtt caataacatt tttccccttg acatggagta gcagggtttt tttttattag 1140  
 atattttctt tactttacatt tcaaattgcta tcccgaataat tccctgtacc ctctccctgt 1200  
 cctgttcccc taccacacca ctcccacttc ttggccctgg cattcccctg gagtatcagt 1260  
 tttttattag tcaaaactatc tcaactgacta agggtcataa aacaagttat tttaacacta 1320  
 atttcaatta aatcaaaggt aaagtgtcag cacatgcctt taatcacaca attccatcaa 1380  
 attcagcact caggagaggg tgatctctgt gaattccagc acactggcgg ccgttactag 1440  
 tggatccgag ctcggtacca agctt 1465

<210> 153  
 <211> 311  
 <212> .PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R25 (mGR25)

<400> 153  
 Met Met Gly Ile Ala Ile Asp Ile Leu Trp Ala Ala Ile Ile Ile Val  
 1 5 10 15  
 Gln Phe Ile Ile Gly Asn Ile Ala Asn Gly Phe Ile Ala Leu Val Asn  
 20 25 30  
 Ile Ile Asp Trp Val Lys Arg Arg Lys Ile Ser Leu Met Asp Lys Ile  
 35 40 45  
 Ile Thr Ala Leu Ala Ile Ser Arg Ile Tyr Leu Leu Trp Ser Thr Phe  
 50 55 60  
 Leu Ile Thr Leu Thr Ser Ser Leu Asp Pro Asp Ile Lys Met Ala Val  
 65 70 75 80  
 Lys Ile Ile Arg Ile Ser Asn Asn Thr Trp Ile Ile Ala Asn His Phe  
 85 90 95  
 Ser Ile Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe Leu Lys Ile  
 100 105 110  
 Ala Asn Phe Ser Asn Tyr Ile Phe Leu Tyr Leu Arg Trp Arg Phe Lys  
 115 120 125  
 Lys Val Val Ser Val Thr Leu Leu Ile Ser Leu Ile Phe Leu Leu Leu  
 130 135 140  
 Asn Ile Leu Leu Met Asn Met His Ile Asp Ile Trp Ser Asp Lys Ser  
 145 150 155 160  
 Lys Arg Asn Leu Ser Phe Ser Val Arg Ser Asn Asn Cys Thr Gln Phe  
 165 170 175  
 Pro Arg Leu Val Leu Leu Ile Asn Thr Met Phe Thr Ser Ile Pro Phe  
 180 185 190  
 Thr Val Ser Leu Leu Ala Phe Leu Leu Leu Ile Phe Ser Leu Trp Arg  
 195 200 205  
 His Leu Lys Thr Met Gln Tyr Tyr Ala Lys Gly Ser Glu Asp Thr Thr  
 210 215 220

Thr Ala Ala His Ile Lys Ala Leu His Met Val Val Ala Phe Leu Leu  
 225 230 235 240  
 Phe Tyr Thr Val Phe Phe Leu Ser Leu Ala Ile Gln Tyr Trp Thr Ser  
 245 250 255  
 Gly Ser Gln Glu Asn Asn Asn Leu Phe Tyr Ala Thr Ile Val Ile Thr  
 260 265 270  
 Phe Pro Ser Val His Ser Cys Ile Leu Ile Leu Arg Asn Ser Gln Leu  
 275 280 285  
 Arg Gln Ala Ser Leu Leu Val Leu Trp Trp Leu Leu Cys Lys Ser Lys  
 290 295 300  
 Asp Val Arg Met Leu Val Pro  
 305 310

<210> 154  
 <211> 1103  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R25 (mGR25)

<400> 154  
 aaaactattc gaattgaaca cagtaaccaa ttcttcagcg gacttacaca aatcaagcta 60  
 ttatcttatg gatgatgggt attgccatag atatcttatg ggcagctatt atcattgtgc 120  
 aattcataat tgggaatatt gcaaattggat tcatagcatt ggtgaacatc atagactggg 180  
 tgaagagaag aaaaatctct ttaatggata agatcattac tgctttggca atctctagga 240  
 tttatctgct gtggtctaca ttcttaatta cactaacatc ttactggat ccagatatta 300  
 aaatggctgt gaaaatcatt agaataagca ataacacctg gattattgca aatcatttca 360  
 gcatttggtt tgctacatgt ctcagcatct tttatcttct caagatagcc aatttttcta 420  
 actatatttt tctctactta aggtggagat ttaagaagggt ggtttcagtg acattgctaa 480  
 tctctcttat ctctctgctt ttaaataattt tactgatgaa catgcatatt gatattctgga 540  
 gtgataagtc caaaagaaac ctttctttta gtgtcagatc aaataattgc actcagtttc 600  
 ccagacttgt ccttttaate aacacaatgt tcacatcaat ccccttcact gtgtccctgt 660  
 tggcttttct gcttctcatc ttctccctgt ggagacacct gaaaaccatg caatactatg 720  
 ctaaaggctc cgaagacacc accacagctg cacatataaa ggccttgac atggtagtgg 780  
 cctttctcct gttctacaca gttttctttt tgtctcttgc catacaatat tggacctctg 840  
 ggtctcaaga gaataacaac ctgttttatg ccacaattgt aattactttc ccttcagtcc 900  
 attcatgtat cctgattctg agaaacagcc agctgaggca ggcattctctg ttggtgctgt 960  
 ggtggctgct gtgcaagtcc aaagatgtac ggatgttggt tccctgaaat actctgtcaa 1020  
 tgctcttttag tagtgaagaa gaaaatagct tagttaagga aattcttggt cattaccgaa 1080  
 gtatactttc aagtttatgt atc 1103

<210> 155  
 <211> 308  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R26 (mGR26)

<400> 155  
 Met Leu Pro Thr Leu Ser Val Phe Phe Met Leu Thr Phe Val Leu Leu  
 1 5 10 15

Cys Phe Leu Gly Ile Leu Ala Asn Gly Phe Ile Val Leu Met Leu Ser  
                   20                                  25                                  30  
 Arg Glu Trp Leu Leu Arg Gly Arg Leu Leu Pro Ser Asp Met Ile Leu  
                   35                                  40                                  45  
 Phe Ser Leu Gly Thr Ser Arg Phe Phe Gln Gln Cys Val Gly Leu Val  
                   50                                  55                                  60  
 Asn Ser Phe Tyr Tyr Phe Leu His Leu Val Glu Tyr Ser Gly Ser Leu  
                   65                                  70                                  75                                  80  
 Ala Arg Gln Leu Ile Ser Leu His Trp Asp Phe Leu Asn Ser Ala Thr  
                                   85                                  90                                  95  
 Phe Trp Phe Cys Thr Trp Leu Ser Val Leu Phe Cys Ile Lys Ile Ala  
                   100                                  105                                  110  
 Asn Phe Ser His Pro Ala Phe Leu Trp Leu Lys Trp Arg Phe Pro Ala  
                   115                                  120                                  125  
 Leu Val Pro Trp Phe Leu Leu Gly Ser Ile Leu Val Ser Val Ile Val  
                   130                                  135                                  140  
 Thr Leu Leu Phe Phe Trp Gly Asn His Thr Ile Tyr Gln Ala Phe Leu  
                   145                                  150                                  155                                  160  
 Arg Arg Lys Phe Thr Gly Asn Thr Thr Phe Lys Glu Trp Asn Arg Arg  
                                   165                                  170                                  175  
 Leu Glu Ile Asp Tyr Phe Met Pro Leu Lys Val Val Thr Met Ser Ile  
                   180                                  185                                  190  
 Pro Cys Ser Leu Phe Leu Val Ser Ile Leu Leu Leu Ile Ser Ser Leu  
                   195                                  200                                  205  
 Arg Arg His Ser Leu Arg Met Gln His Asn Thr His Ser Leu Gln Asp  
                   210                                  215                                  220  
 Pro Asn Val Gln Ala His Ser Arg Ala Leu Lys Ser Leu Ile Ser Phe  
                   225                                  230                                  235                                  240  
 Leu Val Leu Tyr Ala Val Ser Phe Val Ser Met Ile Ile Asp Ala Thr  
                                   245                                  250                                  255  
 Val Phe Ile Ser Ser Asp Asn Val Trp Tyr Trp Pro Trp Gln Ile Ile  
                   260                                  265                                  270  
 Leu Tyr Phe Cys Met Ser Val His Pro Phe Ile Leu Ile Thr Asn Asn  
                   275                                  280                                  285  
 Leu Arg Phe Arg Gly Thr Phe Arg Gln Leu Leu Leu Leu Ala Arg Gly  
                   290                                  295                                  300  
 Phe Trp Val Ala  
 305

<210> 156  
 <211> 3437  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R26 (mGR26)

<400> 156  
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 aaaataagtc aaaatcacag tgatgttact agggatctag gataagggaa tgaagagaaa 120  
 gatgttggtc atagagtaca aaaattcagc taagaactca gtcctggagg ctgaatgtat 180  
 agctgtgtga cagacagcag ctagccatac cagagtatac acttgccctc tgctgaaaga 240  
 gtagatctta tgtgtccttg tcacacataa aagtaattga aaaagtaact ctctgagatg 300  
 acagatacgt taaaatgggt ttacttttca acctgctcca gtaggggtcc ctttaatgtt 360  
 tgtgctagta gatgggggac tctcaagtat ctttgtggta gacaaatcta aggtggcctt 420  
 catgaatacc aaccagact tttgtgactt tgtgatcccc cacttttgaa gtggataaga 480  
 gctgtgactt gagtctaate aaaggagtc aacgtgttgt ttattctgta acagtgcctt 540  
 gtgtttctag ttaataacac aggc aaagaa ggctaggggtg acattcctag gatttgttta 600  
 tttctatctt gctcatgctt cctctgtctg gtctaatagaa ataagtcagt ggccatattt 660  
 aaatatgact acgtggcaaa tactgatgat agcctgtgtg ttccaacaaa tatccagtag 720  
 gagacctagg cattcagtc tgcagccaca aggaaatagg ttcttttact ggaaaaagag 780  
 cagtttagat gggtataaat tacttaatac atagaagcca taggggcttt atgtagagat 840  
 ttgggtagag aggtagacct agatattgac ttaggagtgg ctattcctga gtgggggtag 900  
 atatatggca gggaaactca gataagaaag acttctttag tgtcacgatt tttcctaggt 960  
 atctccttgt gccagatata tatgcgtcta tgtacctacc tacctaccta cctacctacc 1020  
 tacctaccta cctactgaca cctaataagga agaggcaagt ggtcacaacc tgcaatgatg 1080  
 ggataagaat gatggaactc agttaccaag attaaaatac cttccccact gatgttattg 1140  
 caagcatggc agcatgtagg caaaatcaga gaaggcaaat catgagcagc tgctgcccc 1200  
 tggtagcccg gcccgga aaaatctgcat atacttgagc caaaagcaca ccttttatct 1260  
 actgctcgag catttttcc attgaagttc tggctcacat gcagaatcca accatttatc 1320  
 tctgtctc agagggtg gtcagggact gtgggtaggg gcaggaggga ggccaggaa 1380  
 caaggcaatc agtgggtgaca ggaggaggga ctgaaatgct accaacatta tcagttttct 1440  
 tcatgttgac ctttgttctg ctctgtttcc tggggatcct ggccaacggc ttcattgtgc 1500  
 tgatgctgag cagggaatgg ctactgcgtg gtaggctgct cccctcggac atgatcctct 1560  
 tcagtttggg cacctcccga ttcttcagc agtgtgtggg attggtcaac agtttctatt 1620  
 acttctcca tctggttgag tactccggga gccttgccc gcagctcatt agtcttctact 1680  
 gggacttctt gaactcagcc actttctggt tttgtacctg gctcagcgtc ctgttctgta 1740  
 tcaagattgc taacttctc catcctgcct tctgtgtggt gaagtggaga ttcccagcgt 1800  
 tgggtgccctg gtctctgttg ggctctatct tgggtccgt cattgtaact ctgctgttct 1860  
 tttggggaaa ccacactata tatcaggcat tcttaaggag aaagtttact gggaacacaa 1920  
 cctttaagga gtggaacaga aggttggaat tagactattt catgcctctg aaagttgtca 1980  
 ccatgtcaat tcttgttct ctttttctg tctcaatttt gctgttgatc agttctctca 2040  
 gaaggcattc gctaagaatg cagcacataa cccacagctt gcaagacccc aacgtccagg 2100  
 ctcacagcag agccctgaag tcatcctct cattcctggg tctttatgag gtgtcctttg 2160  
 tgtccatgat cattgatgct acagtcttca tctcctcaga taatgtgtgg tattggccct 2220  
 ggcaaatat actttacttt tgcatgtctg tacatccatt taccctcatc accaataatc 2280  
 tcaggttccg cggcaccttc aggcagctac tctgtgtggc caggggattc tgggtggcct 2340  
 agaaggcttg gtctctttat cttagagcct tgaagagact caggtgaggg taacttcact 2400  
 tgggaagtga ctcactctac tggaaatgtc tttgtaggca ggcatggggc catactgtga 2460  
 gggtcctcat tgggaaagag gagaagaaaa tacagagtgt ccttctctac cttaggatat 2520  
 tatgaaagtg gaaattccga atcctggacc agtattgac taagtcaaaa gtacaatatg 2580  
 tctgttctc ttcatgtctg ttttctttt gttactgatt cattctctag ggaatagtct 2640  
 tgatcaactg aatcatctca tctggctggc cactggggag gtaaaagaac tttgtgtcac 2700  
 tgctgcattg ggatatacat ggggtgggaag caagtgtccc tgaggcagag tagcactcag 2760  
 tatgagaacc tcaaaagaca ggtggctgtg catgcagggg ctggggcaag gactcctgat 2820  
 cactcttcac tgtatgggga ttatttgtct ttgtccaaaa tttggagact ttggctttag 2880  
 tttgtggaag atgactggaa aaattcttaa tctaccctg tatcatttct caataatatt 2940  
 ttccttttcc tgcctttaat tttctctat ctgcagcgcc ccttgcttgt tatccgtaaa 3000  
 taaataaata aataaataaa taagcccaat cctcattttc ctgtcttttg gaaccctttt 3060  
 acttccccag gtatacgcta caaagccact tctgcattga ataaacatta tctttcattc 3120

agaaaaagac ttaagaatct cacctttaca aaaaaaaaaa aaaaagaatc tcacttattt 3180  
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 ataaaaataa cttgctctaa gaattataca aatgttttga aaggtaactt tggaaaaaaa 3300  
 gtgtgattag acatggatgt ttgtaagaca gaacaaagag ctcttggaag tccatggcag 3360  
 ctcattggtc ttgccttcag tagagcctgt ctgaatcctg taacctctta tgcccttttg 3420  
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<210> 157  
 <211> 340  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R27 (mGR27)

<400> 157  
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 atttgtctat tgtgcgtaat actattagat tgttttatat tggtgctata tccagatgtc 180  
 tatgccactg gtaaagaaat gagaatcatt gacttcttct ggacactaac caatcactta 240  
 agtatctggg ttgcaacctg cctcagcatt tactatttct tcaagatagg taatttcttt 300  
 caccacttt tcctatgcct caagtctaga cgccaagggc 340

<210> 158  
 <211> 82  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R28 (mGR28)

<400> 158  
 Gly Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile  
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 Leu Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr  
 20 25 30  
 Val His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly  
 35 40 45  
 Leu Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala  
 50 55 60  
 Thr Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile  
 65 70 75 80  
 Ala Asn

<210> 159  
 <211> 341  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R28 (mGR28)

<400> 159  
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cactccacct tcctgtgtct caagtctaga cgccaagggc g 341

<210> 160  
<211> 320  
<212> PRT  
<213> Mus sp.

<220>  
<223> mouse T2R29 (mGR29)

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20 25 30  
Ile His Trp Tyr Lys Arg Arg Lys Ile Ser Ala Leu Asn Gln Ile Leu  
35 40 45  
Thr Ala Leu Ala Phe Ser Arg Ile Tyr Leu Leu Leu Thr Val Phe Thr  
50 55 60  
Val Ile Ala Val Ser Thr Leu Tyr Thr His Val Leu Val Thr Arg Arg  
65 70 75 80  
Val Val Lys Leu Ile Asn Phe His Leu Leu Phe Ser Asn His Phe Ser  
85 90 95  
Met Trp Leu Ala Ala Cys Leu Gly Leu Tyr Tyr Phe Leu Lys Ile Ala  
100 105 110  
His Phe Pro Asn Ser Ile Phe Val Tyr Leu Lys Met Arg Ile Asn Gln  
115 120 125  
Val Val Ser Gly Thr Leu Leu Met Ser Leu Gly Leu Leu Phe Leu Asn  
130 135 140  
Thr Leu Leu Ile Asn Ser Tyr Ile Asp Thr Lys Ile Asp Asp Tyr Arg  
145 150 155 160  
Glu His Leu Leu Tyr Asp Phe Thr Ser Asn Asn Thr Ala Ser Phe Tyr  
165 170 175  
Arg Val Ile Leu Val Ile Asn Asn Cys Ile Phe Thr Ser Ile Pro Phe  
180 185 190  
Thr Leu Ser Gln Ser Thr Phe Leu Leu Leu Ile Phe Ser Leu Trp Arg  
195 200 205  
His Tyr Lys Lys Met Gln Gln His Ala Gln Arg Cys Arg Asp Val Leu  
210 215 220

Ala Asp Ala His Ile Arg Val Leu Gln Thr Met Val Thr Tyr Val Leu  
 225 230 235 240

Leu Cys Ala Ile Phe Phe Leu Ser Leu Ser Met Gln Ile Leu Arg Ser  
 245 250 255

Glu Leu Leu Lys Asn Ile Leu Tyr Val Arg Phe Cys Glu Ile Val Ala  
 260 265 270

Ala Val Phe Pro Ser Gly His Ser Cys Val Leu Ile Cys Arg Asp Thr  
 275 280 285

Asn Leu Arg Gly Thr Phe Leu Ser Val Leu Ser Trp Leu Lys Gln Arg  
 290 295 300

Phe Thr Ser Trp Ile Pro Asn Ile Asn Cys Arg Ser Ser Cys Ile Phe  
 305 310 315 320

<210> 161  
 <211> 1108  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R29 (mGR29)

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 ttgccttaca gacaatggat ggaatcgtac agaactggt tacattcatt gtaattgtgg 180  
 aaataataat aggatggatt ggaaatggat tcatagctct ggtgaactgc atacactggt 240  
 acaagagaag aaagatctct gcaactgaatc aaatactcac agccttggct ttctccagaa 300  
 tctaccttct tttaacagta ttactgtta tagcagtgtc tacgctatac acacacgtgt 360  
 tggttaactag aagagtggta aaactgatta atttccattt gcttttcagc aatcatttta 420  
 gcatgtggct tgctgcatgc cttggccttt attattttct taaaatagct ctttttccta 480  
 actctatttt tgtttactta aagatgagaa ttaaccaggt ggtttcaggg actttgctca 540  
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<210> 162  
 <211> 312  
 <212> PRT  
 <213> Mus sp.

<220>  
 <223> mouse T2R30 (mGR30)

<400> 162  
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 Met Gly Trp Met Lys Asn Arg Lys Ile Ala Ser Ile Asp Leu Ile Leu  
 35 40 45  
 Ser Ser Val Ala Met Ser Arg Ile Cys Leu Gln Cys Ile Ile Leu Leu  
 50 55 60  
 Asp Cys Ile Ile Leu Val Gln Tyr Pro Asp Thr Tyr Asn Arg Gly Lys  
 65 70 75 80  
 Glu Met Arg Thr Val Asp Phe Phe Trp Thr Leu Thr Asn His Leu Ser  
 85 90 95  
 Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Leu Phe Lys Ile Ala  
 100 105 110  
 Asn Phe Phe His Pro Leu Phe Leu Trp Ile Lys Trp Arg Ile Asp Lys  
 115 120 125  
 Leu Ile Leu Arg Thr Leu Leu Ala Cys Val Ile Ile Ser Leu Cys Phe  
 130 135 140  
 Ser Leu Pro Val Thr Glu Asn Leu Ser Asp Asp Phe Arg Arg Cys Val  
 145 150 155 160  
 Lys Thr Lys Glu Arg Ile Asn Ser Thr Leu Arg Cys Lys Val Asn Lys  
 165 170 175  
 Ala Gly His Ala Ser Val Lys Val Asn Leu Asn Leu Val Met Leu Phe  
 180 185 190  
 Pro Phe Ser Val Ser Leu Val Ser Phe Leu Leu Leu Ile Leu Ser Leu  
 195 200 205  
 Trp Arg His Thr Arg Gln Ile Gln Leu Ser Val Thr Gly Tyr Lys Asp  
 210 215 220  
 Pro Ser Thr Thr Ala His Val Lys Ala Met Lys Ala Val Ile Ser Phe  
 225 230 235 240  
 Leu Ala Leu Phe Val Val Tyr Cys Leu Ala Phe Leu Ile Ala Thr Ser  
 245 250 255  
 Ser Tyr Phe Met Pro Glu Ser Glu Leu Ala Val Ile Trp Gly Glu Leu  
 260 265 270  
 Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly  
 275 280 285  
 Ser Ser Lys Leu Lys Gln Ala Ser Val Arg Val Leu Cys Arg Val Lys  
 290 295 300  
 Thr Met Leu Lys Gly Lys Lys Tyr  
 305 310



<210> 163  
 <211> 3775  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R30 (mGR30)

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 caaatagtag ctcagcctaa attaactgtg tgtagaaaag aatgacctgc ggagaagata 240  
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 gatttagata aactatctac agtcttcatg tataattctc atcttcatca caagacagac 360  
 ttcaacttaa ggaggtaaag acaaggacag cgaaccctaa acagccaagt gtagaaacca 420  
 aactgcatca aatcagccag aaactaattg gatacttctc tacttttaaaa tgacatacga 480  
 aacagatact accttaatgc ttgtagctgt tgggtgaggcc ttagtaggga ttttaggaaa 540  
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<210> 164

<211> 310

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R31 (mGR31)

<400> 164

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Asn Met Phe Ile Gly Leu Ala Asn Cys Ser Asp Trp Val Lys Asn Gln
      20              25              30

```

```

Lys Ile Thr Phe Ile Asn Phe Ile Met Val Cys Leu Ala Ala Ser Arg
    35              40              45

```

```

Ile Ser Ser Val Leu Met Leu Phe Ile Asp Ala Thr Ile Gln Glu Leu
    50              55              60

```

```

Ala Pro His Phe Tyr Tyr Ser Tyr Arg Leu Val Lys Cys Ser Asp Ile
    65              70              75              80

```

```

Phe Trp Val Ile Thr Asp Gln Leu Ser Thr Trp Leu Ala Thr Cys Leu
      85              90              95

```

```

Ser Ile Phe Tyr Leu Phe Lys Val Ala His Ile Ser His Pro Leu Phe
    100              105              110

```

```

Leu Trp Leu Lys Trp Arg Leu Arg Gly Val Leu Val Val Phe Leu Val
    115              120              125

```

```

Phe Ser Leu Phe Leu Leu Ile Ser Tyr Phe Leu Leu Leu Glu Thr Leu
    130              135              140

```

```

Pro Ile Trp Gly Asp Ile Tyr Val Thr Leu Lys Asn Asn Leu Thr Leu
    145              150              155              160

```

```

Phe Ser Gly Thr Ile Lys Thr Thr Ala Phe Gln Lys Ile Ile Val Phe
    165              170              175

```

```

Asp Ile Ile Tyr Leu Val Pro Phe Leu Val Ser Leu Ala Ser Leu Leu
    180              185              190

```

```

Leu Leu Phe Leu Ser Leu Val Lys His Ser Arg Ser Leu Asp Leu Ile
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Ser Thr Thr Ser Glu Asp Ser Arg Thr Lys Ile His Lys Lys Ala Met  
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 Lys Met Leu Val Ser Phe Leu Ile Leu Phe Ile Ile His Ile Phe Phe  
 225 230 235 240  
 Met Gln Leu Ala Arg Trp Leu Leu Phe Leu Phe Pro Met Ser Arg Pro  
 245 250 255  
 Ile Asn Phe Ile Leu Thr Leu Asn Ile Phe Ala Leu Thr His Ser Phe  
 260 265 270  
 Ile Leu Ile Leu Gly Asn Ser Asn Leu Arg Gln Arg Ala Met Arg Ile  
 275 280 285  
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 290 295 300  
 Arg Phe Ser Ser Leu Tyr  
 305 310

<210> 165  
 <211> 4675  
 <212> DNA  
 <213> Mus sp.

<220>  
 <223> mouse T2R31 (mGR31)

<220>  
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gaaggatatt	atctcacagt	ctggttataa	aacacaaacc	aatcttttta	taatttcttt	2940
acagcattgc	taataaaaga	cttgtagtct	caaataattt	aaagagaata	attaatttta	3000
taggcaaaag	gtatgaaatt	acaattcaca	gggaagggtc	atgactcctt	agatattaaa	3060
gttaattgta	agccacaata	ggcagaagat	gagcaaaatg	ttgataggag	ataaataaaa	3120
tctaaagtta	cggagaaaaa	aaacatcaac	ttgcctttta	gattacttta	aagctctctc	3180
tctcgtctct	tctctctgta	tctacttact	ttatatatac	aaatgttttg	tctgcatgta	3240
tttctttgca	ccatataaat	gtctaagtat	ccagaangtc	agcagagggc	atcaaattct	3300
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ctctgccaca	gcaactgctc	ttccctgctg	agtcatgttt	taagtctcca	caacttaaac	3420
tcattgttga	tgtggctcatt	gcataatgat	gaattttacat	tctaagggtt	gtatcatagg	3480
taggagggct	ggtttttaac	atattctaat	gttcttatac	aaaccaggt	tttgtaagag	3540
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gaggggaatt	ttatacagtg	taccctgata	acccttgctt	cccactcctt	gcagggtctac	3660
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taagctgcct	ccccaccact	accaccatag	ggcattaact	gtgaagagct	acacttttagc	3840
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tctcagttaa	agtcactgc	aaaagaagtc	tgctggctct	aataaaagctt	gcaacagcat	4020
gggccagtga	catcatcatg	atttctggca	acaatatgga	ccacaaatat	catggctcag	4080
gtggcattac	ggaccacaga	catcaacatg	gtctctggca	gcaagaacca	gaatcttttg	4140
aggaggcttc	attcagaaaa	tgaatttttc	ttcatcccag	atatactgat	gttgctcaat	4200
cagagtatta	gtatggttgg	gcacatattt	tggggacagg	accttcaata	tttccaggct	4260
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tatgcgcctg	tgggcagaaa	tacatctttg	tactttctta	cacctagcag	ggtgagtagc	4380
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gtctgcactg	ccatatctat	ggctgggttct	ccatccctag	ttctgcttct	ctcagggtttt	4560
atacgactct	attccacatt	ctatttttcc	agttccatga	aaccagtggt	taaaagtatc	4620
atcccataag	accggccttt	taaagggttat	tctggagata	ttgcagagtc	tgcag	4675

<210> 166

<211> 20

<212> PRT

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:T2R family
        consensus sequence 1, T2R transmembrane region 1

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Phe or Ala

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Ile, Val or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Val or Leu

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Leu or Val

<220>
<221> MOD_RES
<222> (10)
<223> Xaa = Gly or Thr

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Val or Ala

<220>
<221> MOD_RES
<222> (18)
<223> Xaa = Ile or Met

<400> 166
Glu Xaa Xaa Xaa Gly Xaa Xaa Gly Asn Xaa Phe Ile Xaa Leu Val Asn
  1             5             10             15

Cys Xaa Asp Trp
      20

<210> 167
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
        consensus sequence 2, T2R transmembrane region 2

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<220>
<221> MOD_RES
<222> (1)
<223> Xaa = Asp or Gly

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Phe or Leu

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Ile or Leu

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Thr or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Gly, Ala or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Cys, Gly or Phe

<400> 167
Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu
  1             5             10

<210> 168
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
      consensus sequence 3, T2R transmembrane region 3

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Leu or Phe

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Ser, Thr or Asn

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Leu, Ile or Val

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<220>  
<221> MOD\_RES  
<222> (7)  
<223> Xaa = Phe or Leu

<220>  
<221> MOD\_RES  
<222> (8)  
<223> Xaa = Ala or Thr

<220>  
<221> MOD\_RES  
<222> (10)  
<223> Xaa = Cys, Ser or Asn

<220>  
<221> MOD\_RES  
<222> (12)  
<223> Xaa = Ser, Asn or Gly

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Xaa = Ile or Val

<400> 168  
Asn His Xaa Xaa Xaa Trp Xaa Xaa Thr Xaa Leu Xaa Xaa  
1 5 10

<210> 169  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:T2R family  
consensus sequence 4, T2R transmembrane region 4

<220>  
<221> MOD\_RES  
<222> (3)  
<223> Xaa = Phe or Cys

<220>  
<221> MOD\_RES  
<222> (8)  
<223> Xaa = Asn or Ser

<220>  
<221> MOD\_RES  
<222> (11)  
<223> Xaa = His or Asn

<220>  
<221> MOD\_RES  
<222> (12)  
<223> Xaa = Pro or Ser

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Xaa = Leu, Ile or Val

<220>  
<221> MOD\_RES  
<222> (16)  
<223> Xaa = Trp or Tyr

<400> 169  
Phe Tyr Xaa Leu Lys Ile Ala Xaa Phe Ser Xaa Xaa Xaa Phe Leu Xaa  
1 5 10 15

Leu Lys

<210> 170  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:T2R family  
consensus sequence 5, T2R transmembrane region 5

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Xaa = Ile, Phe or Val

<220>  
<221> MOD\_RES  
<222> (8)  
<223> Xaa = Lys or Arg

<220>  
<221> MOD\_RES  
<222> (10)  
<223> Xaa = Ser or Thr

<220>  
<221> MOD\_RES  
<222> (11)  
<223> Xaa = Lys or Arg

<220>  
<221> MOD\_RES  
<222> (12)  
<223> Xaa = Gln or Lys

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Xaa = Met or Ile

<220>  
<221> MOD\_RES  
<222> (14)  
<223> Xaa = Gln or Lys



<400> 170  
Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa Xaa  
1 5 10

<210> 171  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:T2R family  
consensus sequence 6, T2R transmembrane region 7

<220>  
<221> MOD\_RES  
<222> (3)  
<223> Xaa = Phe or Leu

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Xaa = Ile or Val

<220>  
<221> MOD\_RES  
<222> (7)  
<223> Xaa = Leu or Met

<220>  
<221> MOD\_RES  
<222> (8)  
<223> Xaa = Gly, Ser or Thr

<220>  
<221> MOD\_RES  
<222> (10)  
<223> Xaa = Pro, Ser or Asn

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Xaa = Lys or Arg

<220>  
<221> MOD\_RES  
<222> (14)  
<223> Xaa = Gln or Arg

<400> 171  
His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa  
1 5 10

<210> 172  
<211> 300  
<212> PRT  
<213> Mus sp.

<220>  
<223> mT2R5

<220>  
 <221> MOD\_RES  
 <222> (44)  
 <223> Xaa = Ile or Thr

<220>  
 <221> MOD\_RES  
 <222> (85)  
 <223> Xaa = Val or Ile

<220>  
 <221> MOD\_RES  
 <222> (101)  
 <223> Xaa = Ala or Thr

<220>  
 <221> MOD\_RES  
 <222> (155)  
 <223> Xaa = Asp or Gly

<220>  
 <221> MOD\_RES  
 <222> (294)  
 <223> Xaa = Arg or Leu

<400> 172  
 Met Leu Ser Ala Ala Glu Gly Ile Leu Leu Ser Ile Ala Thr Val Glu  
 1 5 10 15  
 Ala Gly Leu Gly Val Leu Gly Asn Thr Phe Ile Ala Leu Val Asn Cys  
 20 25 30  
 Met Asp Trp Ala Lys Asn Asn Lys Leu Ser Met Xaa Gly Phe Leu Leu  
 35 40 45  
 Ile Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Leu Leu Thr Leu  
 50 55 60  
 Asp Ala Tyr Ala Lys Leu Phe Tyr Pro Ser Lys Tyr Phe Ser Ser Ser  
 65 70 75 80  
 Leu Ile Glu Ile Xaa Ser Tyr Ile Trp Met Thr Val Asn His Leu Thr  
 85 90 95  
 Val Trp Phe Ala Xaa Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala  
 100 105 110  
 Asn Phe Ser Asp Cys Val Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys  
 115 120 125  
 Ala Phe Val Phe Leu Leu Gly Cys Leu Leu Thr Ser Trp Val Ile Ser  
 130 135 140  
 Phe Ser Phe Val Val Lys Val Met Lys Asp Xaa Lys Val Asn His Arg  
 145 150 155 160  
 Asn Arg Thr Ser Glu Met Tyr Trp Glu Lys Arg Gln Phe Thr Ile Asn  
 165 170 175  
 Tyr Val Phe Leu Asn Ile Gly Val Ile Ser Leu Phe Met Met Thr Leu  
 180 185 190

Thr	Ala	Cys	Phe	Leu	Leu	Ile	Met	Ser	Leu	Trp	Arg	His	Ser	Arg	Gln
	195						200					205			
Met	Gln	Ser	Gly	Val	Ser	Gly	Phe	Arg	Asp	Leu	Asn	Thr	Glu	Ala	His
	210					215					220				
Val	Lys	Ala	Ile	Lys	Phe	Leu	Ile	Ser	Phe	Ile	Ile	Leu	Phe	Val	Leu
	225				230					235					240
Tyr	Phe	Ile	Gly	Val	Ser	Ile	Glu	Ile	Ile	Cys	Ile	Phe	Ile	Pro	Glu
				245					250					255	
Asn	Lys	Leu	Leu	Phe	Ile	Phe	Gly	Phe	Thr	Thr	Ala	Ser	Ile	Tyr	Pro
		260						265						270	
Cys	Cys	His	Ser	Phe	Ile	Leu	Ile	Leu	Ser	Asn	Ser	Gln	Leu	Lys	Gln
		275					280					285			
Ala	Phe	Val	Lys	Val	Xaa	Gln	Leu	Leu	Lys	Phe	Phe				
	290					295					300				